

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 28, 2005, 13:08:45 ; Search time 16 Seconds
(without alignments)
1942.376 Million cell updates/sec

Title: US-09-978-299A-330
Perfect score: 1694
Sequence: 1 MAAPKGLWVRTQLGLPPLL.....EDHEAGPLPTKVNLAHSEI 323

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB	ID	Description
1	423.5	25.0	342	2	JC7110	brain-specific mem
2	102	6.0	2380	2	T29551	hypothetical prote
3	95.5	5.6	741	2	T46488	hypothetical prote
4	92.5	5.5	858	2	A57513	heat shock protein
5	88.5	5.2	527	2	G71557	probable glucanotr
6	88.5	5.2	817	2	T04697	hypothetical prote
7	87	5.1	736	2	JC7518	subtilisin-like se
8	86.5	5.1	327	2	AC0156	probable cobalamin
9	85.5	5.0	859	2	S66666	heat shock protein
10	85.5	5.0	3225	2	I52300	giantin - human
11	85.5	5.0	3259	1	A56539	giantin - human
12	84.5	5.0	1021	2	T00361	hypothetical prote
13	84	5.0	1312	2	T30845	probable DNA repai
14	84	5.0	1350	2	T13254	nitric-oxide synth
15	83.5	4.9	486	2	S31805	VP5 protein - porc
16	83	4.9	500	2	G72101	conserved hypothet
17	83	4.9	500	2	C86522	hypothetical prote
18	83	4.9	503	2	A81571	hypothetical prote
19	83	4.9	1607	1	MMMSB2	conserved hypothet
20	82	4.8	119	1	MSPG	laminin gamma-1 ch
21	82	4.8	308	2	T33994	motilin precursor
22	82	4.8	626	2	A42891	hypothetical prote
23	81.5	4.8	264	2	JW0022	beta-galactosidase
24	81.5	4.8	566	2	S22477	clt protein - bate
25	81.5	4.8	778	2	H84678	vicilin precursor
26	81	4.8	485	1	S19677	hypothetical prote
27	81	4.8	848	2	C82712	1-aminocyclopropan
28	81	4.8	1032	2	D95177	ATP-dependent seri
29	81	4.8	1032	2	F98043	Snf2 family protei

30	81	4.8	1609	1	MMHUB2
31	80.5	4.8	277	2	T16134
32	80.5	4.8	282	2	JC4134
33	80.5	4.8	459	2	JQ0419
34	80.5	4.8	661	2	B71447
35	80	4.7	491	1	MMXRF
36	80	4.7	614	2	A84152
37	79.5	4.7	264	1	GCBPP4
38	79.5	4.7	600	2	T18593
39	79.5	4.7	827	2	T20492
40	79	4.7	399	2	B69642
41	79	4.7	431	2	F97195
42	79	4.7	487	2	PQ0259
43	79	4.7	545	2	T09195
44	79	4.7	959	2	T25704
45	79	4.7	1122	2	I54237
46	79	4.7	1123	1	JN0712
47	79	4.7	1124	1	S06856
48	79	4.7	1125	1	JH0771
49	78.5	4.6	193	2	E83864
50	78.5	4.6	668	2	T26724
51	78.5	4.6	1449	2	A12017
52	78	4.6	564	2	T21423
53	78	4.6	624	2	T41341
54	77.5	4.6	166	2	AH2315
55	77.5	4.6	287	2	T39197
56	77.5	4.6	462	2	A48933
57	77.5	4.6	464	2	B34130
58	77.5	4.6	646	2	T27899
59	77.5	4.6	669	2	T08960
60	77.5	4.6	696	2	E96831
61	77.5	4.6	800	2	H83691
62	77.5	4.6	890	2	AH0528
63	77.5	4.6	1259	2	S36126
64	77	4.5	330	2	E82063
65	77	4.5	364	2	T08903
66	77	4.5	475	2	T46745
67	77	4.5	661	2	T42754
68	77	4.5	714	2	S68603
69	77	4.5	719	2	S62466
70	77	4.5	747	2	S35546
71	77	4.5	878	2	B71460
72	76.5	4.5	363	2	F97899
73	76.5	4.5	449	2	D86231
74	76.5	4.5	471	2	S45068
75	76.5	4.5	569	2	E90554
76	76.5	4.5	657	2	S25184
77	76.5	4.5	1965	2	T33216
78	76.5	4.5	2895	2	T08437
79	76.5	4.5	3328	2	T30835
80	76	4.5	277	2	I83570
81	76	4.5	375	2	AC1350
82	76	4.5	390	2	T10378
83	76	4.5	464	2	S48329
84	76	4.5	572	2	T29880
85	76	4.5	662	2	T23271
86	76	4.5	811	2	S36109
87	76	4.5	830	2	T19283
88	76	4.5	942	2	JC7316
89	76	4.5	1299	2	T42989
90	76	4.5	1471	2	T40117
91	76	4.5	1513	2	T32681
92	76	4.5	1687	2	T30176
93	76	4.5	1828	2	B59254
94	76	4.5	1855	2	A59254
95	76	4.5	2581	2	AF2545
96	75.5	4.5	213	2	B81360
97	75.5	4.5	363	2	D95028
98	75.5	4.5	403	2	T02513
99	75.5	4.5	414	2	E84546
100	75.5	4.5	453	2	T00284
101	75.5	4.5	496	2	JC5261
102	75.5	4.5	754	2	S50601

laminin gamma-1 ch
hypothetical prote
ADP-ribosyl cyclas
coagulation factor
probable GABRA2 -
nonstructural prot
hypothetical prote
clt protein - sate
hypothetical prote
hypothetical prote
flavohemoglobin hm
folylpolyglutamate
hypothetical prote
secy protein homol
hypothetical prote
protein-tyrosine k
phytochrome - gard
protein-tyrosine k
thioredoxin BH1717
hypothetical prote
hypothetical prote
hypothetical prote
probable serine-th
hypothetical prote
yeast atp12 protei
gamma-aminobutyric
gamma-aminobutyric
hypothetical prote
serine/threonine-s
hypothetical prote
hypothetical prote
[protein-Pil] urid
neural cell adhesi
thiamin ABC transp
hypothetical prote
arginine/ornithine
hypothetical prote
hypothetical prote
probable ATP-depen
ATP-dependent RNA
probable outer mem
hypothetical prote
hypothetical prote
53k glycoprotein -
conserved hypothet
cspl protein - Cor
hypothetical prote
hyperplastic discs
breast cancer tumo
hemk protein (BC 1
N-acetylmutamoyl-L
hypothetical prote
probable membrane
hypothetical prote
hypothetical prote
osteoblast-specifi
hypothetical prote
testicular zinc fi
hypothetical prote
myosin-2 isoform -
EGF repeat transme
myosin heavy chain
myosin heavy chain
hypothetical prote
probable protein d
ABC transporter, A
hypothetical prote
probable tetracycl
hypothetical prote
salt-tolerant prot
hypothetical prote

103	75.5	4.5	988	2	E96621	hypothetical prote
104	75.5	4.5	1284	2	T40879	probable helicase
105	75	4.4	277	2	E90843	probable protoporp
106	75	4.4	277	2	B85701	probable protoporp
107	75	4.4	293	2	C90032	hypothetical prote
108	75	4.4	357	2	A12099	WD-40 repeat prote
109	75	4.4	426	2	S16416	gene E46 protein -
110	75	4.4	461	2	C86679	transcription regu
111	75	4.4	486	2	S15470	NS53 protein - hum
112	75	4.4	507	2	E71551	probable monooxyge
113	75	4.4	648	2	JC4674	Sly1 protein - rat
114	75	4.4	775	2	T38352	hypothetical prote
115	75	4.4	893	2	G88551	protein M01A8.2 [i
116	75	4.4	1036	2	S55984	probable membrane
117	75	4.4	1085	2	T18369	K-C1 cotransport p
118	75	4.4	1173	1	A53430	1-phosphatidylinos
119	75	4.4	1216	2	A28822	1-phosphatidylinos
120	75	4.4	1276	2	E96776	hypothetical prote
121	75	4.4	1334	2	E86451	probable copia-tyr
122	75	4.4	1496	2	AH0447	insecticidal toxin
123	74.5	4.4	357	2	T19336	hypothetical prote
124	74.5	4.4	437	2	C97020	argininosuccinate
125	74.5	4.4	472	1	A35327	vitamin D-binding
126	74.5	4.4	500	2	T44167	hypothetical prote
127	74.5	4.4	500	2	T43981	hypothetical prote
128	74.5	4.4	505	1	P1WLP	LI protein - human
129	74.5	4.4	555	2	T23531	hypothetical prote
130	74.5	4.4	673	2	A71978	methyl-accepting c
131	74.5	4.4	728	2	D84647	hypothetical prote
132	74.5	4.4	761	2	T09052	hypothetical prote
133	74.5	4.4	906	2	T47340	hypothetical prote
134	74.5	4.4	1007	2	T47430	disease resistance
135	74.5	4.4	1139	1	E64234	cytadherence-acces
136	74.5	4.4	1342	2	A36223	kinase-related tra
137	74.5	4.4	1630	2	T00390	KIAA0614 protein -
138	74	4.4	243	2	AB1249	3-ketoacyl-acyl ca
139	74	4.4	557	2	T29655	hypothetical prote
140	74	4.4	818	2	H83904	hypothetical prote
141	74	4.4	893	2	T29621	hypothetical prote
142	74	4.4	907	2	T01764	helicase II-like p
143	74	4.4	962	1	JT0669	hypothetical prote
144	74	4.4	1130	2	T20288	sterol regulatory
145	74	4.4	1141	2	A54962	1-phosphatidylinos
146	74	4.4	1216	2	A28821	CL2AA protein - ra
147	74	4.4	1452	2	T17157	CL2AC protein - ra
148	74	4.4	1463	2	T17159	CL2BA protein - ra
149	74	4.4	1467	2	T17160	CL2BC protein - ra
150	74	4.4	1478	2	T17185	alpha-latrotoxin r
151	74	4.4	1487	2	T14324	myosin heavy chain
152	74	4.4	1853	1	A46761	bimE protein - Eme
153	74	4.4	2073	1	BWASBE	genome polypotein
154	74	4.4	2156	1	RVUNE	ankyrin 2, neurona
155	74	4.4	3924	2	S37431	hypothetical prote
156	73.5	4.3	330	2	T25169	H+-transporting tw
157	73.5	4.3	386	2	A39732	sugar ABC transpor
158	73.5	4.3	417	2	AH1170	hypothetical prote
159	73.5	4.3	561	2	T27318	hypothetical prote
160	73.5	4.3	626	2	T27319	methyl-accepting c
161	73.5	4.3	673	1	B64530	hypothetical prote
162	73.5	4.3	711	2	T30107	alpha-glucan synth
163	73.5	4.3	1204	2	S62506	phosphorylase kina
164	73.5	4.3	1235	2	S24109	hypothetical prote
165	73.5	4.3	1414	2	T33236	adenomatous polypo
166	73.5	4.3	2845	2	I49505	breast cancer susc
167	73.5	4.3	3329	2	T42205	probable transcrip
168	73	4.3	298	2	G98159	transcription regu
169	73	4.3	298	2	AB3128	membrane-bound pen
170	73	4.3	366	2	A64950	replicative DNA he
171	73	4.3	446	2	D64210	GABA receptor del
172	73	4.3	449	2	I52630	tubulin gamma chai
173	73	4.3	472	2	S39553	hypothetical prote
174	73	4.3	485	2	G71239	hypothetical prote
175	73	4.3	485	2	C64680	hypothetical prote
176	73	4.3	491	2	A49597	nonstructural prot
177	73	4.3	491	2	S31783	VPS protein - bovi
178	73	4.3	494	2	A89010	protein R08F11.3 [
179	73	4.3	668	1	VCMVFP	env polypotein pr
180	73	4.3	671	1	QRBCSN	two-component sens
181	73	4.3	688	2	T33709	hypothetical prote
182	73	4.3	814	2	D82101	oxidoreductase, ac
183	73	4.3	1014	2	S48235	CIN1 protein - yea
184	73	4.3	1039	2	C64418	isooleucine-tRNA 11
185	73	4.3	1548	2	S34583	serine proteinase
186	73	4.3	1680	2	A43434	furin (EC 3.4.21.7
187	73	4.3	1726	2	T30810	chromatin structur
188	72.5	4.3	177	2	T43665	probable copper ho
189	72.5	4.3	204	2	E65183	hypothetical prote
190	72.5	4.3	242	2	T29699	hypothetical prote
191	72.5	4.3	468	2	T42746	hypothetical prote
192	72.5	4.3	484	2	T04381	NBS-LRR type resis
193	72.5	4.3	504	2	AC2628	ABC transporter, m
194	72.5	4.3	531	2	T29788	phosphate ABC tran
195	72.5	4.3	645	2	S29849	hypothetical prote
196	72.5	4.3	716	2	S30687	gene p74 protein -
197	72.5	4.3	769	2	F81742	hypothetical prote
198	72.5	4.3	843	2	S72375	conserved hypothet
199	72.5	4.3	946	1	A47299	ror-related recept
200	72.5	4.3	1036	2	E84620	hypothetical prote
201	72.5	4.3	1188	2	T41696	probable C2-domain
202	72.5	4.3	1223	2	T17345	hypothetical prote
203	72.5	4.3	1451	1	JQ1719	E2 glycoprotein pr
204	72.5	4.3	222	2	B55356	urokinase-type pla
205	72	4.3	310	2	T46035	AtMYB84 - Arabidop
206	72	4.3	320	2	C90536	lipoprotein [impor
207	72	4.3	330	2	F83955	flagellar motor sw
208	72	4.3	352	2	A97069	cobalamin biosynth
209	72	4.3	360	2	G64575	conserved hypothet
210	72	4.3	379	2	AH1871	two-component resp
211	72	4.3	379	2	A45267	heterocyst pattern
212	72	4.3	387	2	C82545	succinyl-CoA synth
213	72	4.3	430	2	C72014	poly A polymerase
214	72	4.3	430	2	D86611	poly A polymerase
215	72	4.3	430	2	C81526	poly (A) polymerase
216	72	4.3	449	2	A36303	gamma-aminobutyric
217	72	4.3	454	2	T05168	hypothetical prote
218	72	4.3	477	2	T29380	site-specific DNA-
219	72	4.3	499	2	F87373	tryptophan halogen
220	72	4.3	600	1	D65000	NADH2 dehydrogenas
221	72	4.3	654	1	HMIVC8	hemagglutinin prec
222	72	4.3	655	2	S07412	hemagglutinin-este
223	72	4.3	712	2	E86660	HYPOETICAL PROTEI
224	72	4.3	768	2	T17462	disease resistance
225	72	4.3	1069	2	D85383	hypothetical prote
226	72	4.3	1166	2	S33812	myosin-like protei
227	72	4.3	1199	2	T33337	hypothetical prote
228	72	4.3	1411	2	A84460	probable retroelem
229	72	4.3	1784	2	E86921	polyketide synthas
230	72	4.3	3071	2	T50345	vacuolar protein s
231	72	4.3	135	2	T15610	hypothetical prote
232	72	4.3	173	2	T18601	hypothetical prote
233	71.5	4.2	222	2	C91271	urokinase-type pla
234	71.5	4.2	322	2	C86112	phosphatidylserine
235	71.5	4.2	322	2	A29234	phosphatidylserine
236	71.5	4.2	359	2	F91219	hypothetical prote
237	71.5	4.2	359	2	H86065	hypothetical prote
238	71.5	4.2	359	2	S48368	probable membrane
239	71.5	4.2	362	2	T02057	fructose-bisphosph
240	71.5	4.2	400	2	T32705	hypothetical prote
241	71.5	4.2	412	2	C82522	type I restriction
242	71.5	4.2	424	2	D81739	protoporphyryinogen
243	71.5	4.2	428	2	S07916	RF4 protein - yeas
244	71.5	4.2	453	2	S59401	hypothetical prote
245	71.5	4.2	453	2	H70334	hypothetical prote
246	71.5	4.2	621	2		
247	71.5	4.2				
248	71.5	4.2				

249	71.5	4.2	658	2	D69431	methionine-tRNA li	322	70.5	4.2	1805	1	A64224	hypothetical prote
250	71.5	4.2	691	2	A34708	vacuolar protein-s	323	70.5	4.2	1878	2	E86189	hypothetical prote
251	71.5	4.2	745	2	H96760	unknown protein [i	324	70.5	4.2	1942	2	B71426	hypothetical prote
252	71.5	4.2	751	2	F87789	protein C34G6.2 [i	325	70.5	4.2	1984	2	T13171	probable vitelloge
253	71.5	4.2	796	1	JC1285	protein-cytosine-p	326	70.5	4.2	2233	2	T28659	surface protein 51
254	71.5	4.2	861	2	T27164	hypothetical prote	327	70.5	4.2	2843	1	RBHUP	adenomatous polyp
255	71.5	4.2	1056	2	S56039	hypothetical prote	328	70.5	4.2	3329	2	T30904	breast cancer tumo
256	71.5	4.2	1068	2	S64015	pleiotropic drug r	329	70	4.1	191	2	AD0165	probable lipoprote
257	71.5	4.2	1086	2	T33893	hypothetical prote	330	70	4.1	200	2	T01335	hypothetical prote
258	71.5	4.2	1286	2	T18734	hypothetical prote	331	70	4.1	247	2	G82956	hypothetical prote
259	71.5	4.2	2867	2	AG3481	cellobiose-phospho	332	70	4.1	256	2	A81277	probable oxidoredu
260	71	4.2	198	2	AF1870	hypothetical prote	333	70	4.1	269	2	S48978	hypothetical prote
261	71	4.2	220	2	T21730	hypothetical prote	334	70	4.1	271	2	T13013	hypothetical prote
262	71	4.2	234	2	S17956	luxG protein - Pho	335	70	4.1	275	2	A82257	oxidoreductase, sh
263	71	4.2	256	1	DFPG	beta-neoendorphin	336	70	4.1	280	2	H72593	hypothetical prote
264	71	4.2	257	2	E96780	thumatin-like pro	337	70	4.1	328	2	C72386	hypothetical prote
265	71	4.2	307	2	T14823	probable glycoprot	338	70	4.1	373	2	B82697	rod shape-determi
266	71	4.2	327	2	T09027	hypothetical prote	339	70	4.1	449	2	A34625	gamma-aminobutyric
267	71	4.2	332	2	C64073	rbs repressor homo	340	70	4.1	462	2	S53084	gamma-tubulin - Eu
268	71	4.2	366	2	C85800	probable cytochrom	341	70	4.1	521	2	T01212	myc1 protein - Ara
269	71	4.2	366	2	G90951	probable cytochrom	342	70	4.1	578	2	T41715	hypothetical prote
270	71	4.2	455	2	S56695	1-aminocyclopropan	343	70	4.1	585	2	T47364	hypothetical prote
271	71	4.2	482	2	A34924	complement C3b/C4b	344	70	4.1	608	2	T47363	hypothetical prote
272	71	4.2	511	2	E82228	histidine ammonia-	345	70	4.1	640	1	HMIVEA	hemagglutinin prec
273	71	4.2	566	2	S19063	hypothetical prote	346	70	4.1	665	2	H69101	archaeosine tRNA-r
274	71	4.2	600	2	C85869	NADH dehydrogenase	347	70	4.1	727	2	T08920	hypothetical prote
275	71	4.2	600	2	B91025	NADH dehydrogenase	348	70	4.1	790	2	T19040	hypothetical prote
276	71	4.2	640	1	HMIVEB	hemagglutinin prec	349	70	4.1	835	2	T45590	hypothetical prote
277	71	4.2	640	1	HMIVEC	hemagglutinin prec	350	70	4.1	888	2	T01081	hypothetical prote
278	71	4.2	751	2	AD2168	phytochrome-like p	351	70	4.1	956	2	T19046	ras GTPase-activat
279	71	4.2	765	2	A11284	cobalamin-independ	352	70	4.1	1048	2	T31429	ras GTPase-activat
280	71	4.2	776	2	C96554	unknown protein [i	353	70	4.1	1085	2	D89610	ras GTPase-activat
281	71	4.2	836	2	S36110	osteoblast-specifi	354	70	4.1	1137	2	T19042	ras GTPase-activat
282	71	4.2	849	1	S51527	S-receptor kinase	355	70	4.1	1170	2	T19042	ras GTPase-activat
283	71	4.2	943	2	E91286	probable ATP-depen	356	70	4.1	1178	2	S76370	ras GTPase-activat
284	71	4.2	951	2	G82965	conserved hypothet	357	70	4.1	1207	2	T19041	ras GTPase-activat
285	71	4.2	952	2	A86128	probable ATP-depen	358	70	4.1	1259	2	T19043	ras GTPase-activat
286	71	4.2	996	2	B84481	hypothetical prote	359	70	4.1	1322	2	T01842	hypothetical prote
287	71	4.2	1221	2	T30529	ubiquitin carboxyl	360	70	4.1	1358	2	A29360	SIR4 protein - yea
288	71	4.2	1240	2	T04193	hypothetical prote	361	70	4.1	1409	1	OFFFCP	copia polypeptide
289	71	4.2	1453	2	G96613	hypothetical prote	362	70	4.1	1420	2	T17158	CL2AB protein - ra
290	71	4.2	2490	1	A54971	protein-cytosine-p	363	70	4.1	1435	2	T46611	CL2BB protein - ra
291	71	4.2	4717	2	T41581	hypothetical coile	364	70	4.1	1748	2	S63127	probable membrane
292	70.5	4.2	152	2	AE1664	hypothetical prote	365	70	4.1	1810	2	S69973	tyb protein - yea
293	70.5	4.2	334	2	T32256	hypothetical prote	366	70	4.1	1956	2	T16416	hypothetical prote
294	70.5	4.2	411	2	F87644	transcription regu	367	70	4.1	1966	2	T08991	hypothetical prote
295	70.5	4.2	429	1	S16043	threonine synthase	368	70	4.1	2052	2	T37711	probable n-end-rec
296	70.5	4.2	469	2	S44193	tubulin gamma chai	369	70	4.1	2052	2	T18519	myosin X - bovine
297	70.5	4.2	472	1	A53236	transcription fact	370	70	4.1	2493	2	S45734	probable membrane
298	70.5	4.2	474	2	T50558	tubulin gamma-2 ch	371	70	4.1	2531	2	A46012	notch-1 protein -
299	70.5	4.2	496	2	E72032	general secretion	372	69.5	4.1	152	2	AG1292	hypothetical prote
300	70.5	4.2	496	2	F86592	general secretion p	373	69.5	4.1	209	2	T02394	hypothetical prote
301	70.5	4.2	517	2	D86804	sensor protein kin	374	69.5	4.1	294	2	A90542	hypothetical prote
302	70.5	4.2	605	2	A41915	insulin-like growt	375	69.5	4.1	309	2	E96566	F6D8.20 [imported]
303	70.5	4.2	634	2	T41319	conserved hypothet	376	69.5	4.1	353	2	T20656	hypothetical prote
304	70.5	4.2	654	2	T30136	hypothetical prote	377	69.5	4.1	356	2	T20656	hypothetical prote
305	70.5	4.2	662	2	AG2420	hypothetical prote	378	69.5	4.1	358	2	H81618	arginine kinase-re
306	70.5	4.2	665	2	E86775	ribonuclease [limp	379	69.5	4.1	358	2	B86578	arginine kinase [i
307	70.5	4.2	680	2	S17982	Kallmann syndrome	380	69.5	4.1	358	2	E72045	arginine kinase -
308	70.5	4.2	735	2	D70174	methyl-accepting c	381	69.5	4.1	494	2	AD0751	cytoplasmic alpha-
309	70.5	4.2	893	2	E87244	conserved hypothet	382	69.5	4.1	604	2	T34014	hypothetical prote
310	70.5	4.2	909	1	QRXL2	LDL receptor 2 pre	383	69.5	4.1	614	2	PQ0507	polypeptide - deng
311	70.5	4.2	944	2	S56936	vacuolar protein-s	384	69.5	4.1	626	2	T49110	hypothetical prote
312	70.5	4.2	1009	2	T47327	hypothetical prote	385	69.5	4.1	652	2	B84568	probable calmoduli
313	70.5	4.2	1086	2	T14114	K-Cl cotransport p	386	69.5	4.1	728	2	T38220	hypothetical prote
314	70.5	4.2	1120	2	JC7765	mitotic spindle as	387	69.5	4.1	850	2	T14472	S-receptor kinase
315	70.5	4.2	1136	1	USBS81	paraasporal crystal	388	69.5	4.1	851	2	T47305	hypothetical prote
316	70.5	4.2	1142	2	A45031	cysteine-rich fibr	389	69.5	4.1	1001	2	C86181	hypothetical prote
317	70.5	4.2	1180	2	A26858	paraasporal crystal	390	69.5	4.1	1175	2	S52417	E-selectin ligand-
318	70.5	4.2	1180	2	I39870	paraasporal crystal	391	69.5	4.1	1264	2	B84534	probable retroelem
319	70.5	4.2	1279	2	E64709	type IIS restricti	392	69.5	4.1	1358	2	A03905	genome polypeptide
320	70.5	4.2	1553	2	T31436	DNA-directed RNA p	393	69.5	4.1	2120	2	T30243	alpha tectorin - c
321	70.5	4.2	1770	2	S69953	tyb protein - yea	394	69.5	4.1	2787	2	S45416	TEL1 protein - yea

395	69.5	4.1	3137	2	A37797	collagen alpha 3(V
396	69	4.1	217	2	AF1348	competence negativ
397	69	4.1	254	1	DFHU	beta-neoendorphin
398	69	4.1	402	2	T29478	hypothetical prote
399	69	4.1	409	1	D69280	cell division cont
400	69	4.1	421	2	S75494	hypothetical prote
401	69	4.1	436	2	B84071	spore outer layer
402	69	4.1	466	2	B69842	probable oxidoredu
403	69	4.1	520	1	S44099	brain-derived neur
404	69	4.1	523	2	S68517	nuclear hormone re
405	69	4.1	538	1	VCNZMT	cell fusion glycop
406	69	4.1	538	2	S52472	cell fusion protei
407	69	4.1	582	2	D72075	hypothetical prote
408	69	4.1	600	2	AD0797	NADH2 dehydrogenas
409	69	4.1	629	2	F84207	heat shock protein
410	69	4.1	629	2	G81592	hypothetical prote
411	69	4.1	629	2	E86547	hypothetical prote
412	69	4.1	679	2	A40351	adhesion-type prot
413	69	4.1	699	2	T09483	Cys-rich protein R
414	69	4.1	713	2	I50128	fibroblast growth
415	69	4.1	818	1	S44098	brain-derived neur
416	69	4.1	1124	1	I58388	protein-tyrosine k
417	69	4.1	1131	2	JQ0382	phytochrome A - ma
418	69	4.1	1241	2	JU0466	potassium transpor
419	69	4.1	1260	1	S05479	neural cell adhesi
420	69	4.1	1379	2	T45119	FIM protein [impor
421	69	4.1	1446	2	T13018	hypothetical pl prote
422	69	4.1	1770	2	S45842	TYB protein - yeas
423	69	4.1	1819	2	E86410	protein F3M18.14 l
424	69	4.1	2026	1	OYBY	adenylate cyclase
425	69	4.1	2123	2	S55089	probable acetyl-Co
426	69	4.1	2437	2	S42612	transmembrane prot
427	69	4.1	2554	1	TVFE7L	kinase-related pro
428	69	4.1	2910	2	T42214	otogelin - mouse
429	69	4.1	4919	2	T31105	hypothetical prote
430	68.5	4.0	325	2	A40084	exogastrola-induci
431	68.5	4.0	338	2	B83806	transcription regu
432	68.5	4.0	347	2	C64105	o-succinylbenzoate
433	68.5	4.0	355	2	T23406	hypothetical prote
434	68.5	4.0	355	2	F83914	hypothetical prote
435	68.5	4.0	360	2	AE1687	histidinol-phospha
436	68.5	4.0	370	2	F75173	hypothetical prote
437	68.5	4.0	447	2	T49777	probable beta-succ
438	68.5	4.0	486	2	S31808	VP5 protein - huma
439	68.5	4.0	494	2	A42170	zinc finger protel
440	68.5	4.0	521	2	H69317	conserved hypothet
441	68.5	4.0	531	2	T01415	basic leucine zipp
442	68.5	4.0	545	2	H83342	periplasmic trehal
443	68.5	4.0	549	2	G91178	cytoplasmic trehal
444	68.5	4.0	549	2	H86024	cytoplasmic trehal
445	68.5	4.0	549	2	S47739	probable alpha,alp
446	68.5	4.0	575	2	T45668	hypothetical prote
447	68.5	4.0	584	2	S76210	hypothetical prote
448	68.5	4.0	593	2	T04446	hypothetical prote
449	68.5	4.0	607	2	S60658	legumin - Gnetum g
450	68.5	4.0	622	2	F71174	hypothetical prote
451	68.5	4.0	636	2	T10569	probable serine/th
452	68.5	4.0	654	2	T29247	hypothetical prote
453	68.5	4.0	666	2	D42510	Oil protein - vacc
454	68.5	4.0	710	2	T31197	transponson protei
455	68.5	4.0	737	2	S47857	basic protein, cyt
456	68.5	4.0	939	2	S75908	hypothetical prote
457	68.5	4.0	988	2	T51054	related to alpha-a
458	68.5	4.0	1004	2	T00795	26S proteasome reg
459	68.5	4.0	1102	2	T17367	potassium channel
460	68.5	4.0	1104	1	SYBYVT	valine-tRNA ligase
461	68.5	4.0	1170	2	S52525	probable membrane
462	68.5	4.0	1246	2	C36806	hypothetical prote
463	68.5	4.0	1461	2	E84589	probable retroelem
464	68.5	4.0	1570	2	T18272	1-phosphatidylinos
465	68	4.0	127	1	A46528	phosphatidylinosit
466	68	4.0	130	2	I54553	gene TnB protein -
467	68	4.0	167	1	IEECA1	inSB protein - Esc
468	68	4.0	167	2	AB0781	insertion element
469	68	4.0	167	2	AD1041	insertion element
470	68	4.0	167	2	AG0978	insertion element
471	68	4.0	197	2	S28465	quaternary amine t
472	68	4.0	200	2	B54022	ADP-ribosylation f
473	68	4.0	331	2	B89759	conserved hypothet
474	68	4.0	371	2	E71932	probable outer mem
475	68	4.0	396	2	A40066	corticosteroid-bin
476	68	4.0	499	2	T18699	hypothetical prote
477	68	4.0	501	2	S75951	hypothetical prote
478	68	4.0	518	2	A40942	phosphoprotein pho
479	68	4.0	522	2	F97756	hypothetical prote
480	68	4.0	607	2	A95970	conserved hypothet
481	68	4.0	621	2	T39204	hypothetical prote
482	68	4.0	652	2	B70785	probable asparagin
483	68	4.0	683	2	D71680	ribonuclease E (rn
484	68	4.0	693	2	T25878	hypothetical prote
485	68	4.0	734	2	A82047	primosomal replica
486	68	4.0	735	2	AE1858	anthranilate synth
487	68	4.0	802	1	A36065	protein-tyrosine-p
488	68	4.0	829	1	A47373	protein-tyrosine-p
489	68	4.0	1003	2	T24545	hypothetical prote
490	68	4.0	1014	2	T24412	hypothetical prote
491	68	4.0	1300	2	A36502	insulin receptor-x
492	68	4.0	1352	2	F86246	hypothetical prote
493	68	4.0	1352	2	T47925	copia-type polypro
494	68	4.0	1526	2	T19473	hypothetical prote
495	68	4.0	1526	2	T00079	hypothetical prote
496	68	4.0	2338	2	T25810	hypothetical prote
497	68	4.0	2820	2	JC5196	neurofibromin I -
498	67.5	4.0	163	2	B70854	hypothetical prote
499	67.5	4.0	196	2	T26943	hypothetical prote
500	67.5	4.0	215	2	C81731	hypothetical prote
501	67.5	4.0	228	2	B69758	hypothetical prote
502	67.5	4.0	230	2	E86199	hypothetical prote
503	67.5	4.0	248	2	A25530	tropomyosin, fibro
504	67.5	4.0	248	2	S11390	tropomyosin 5 - mo
505	67.5	4.0	248	2	S34124	tropomyosin isofo
506	67.5	4.0	248	2	I53784	tropomyosin - rat
507	67.5	4.0	264	2	E71509	hypothetical prote
508	67.5	4.0	298	2	B34791	interleukin-7 rece
509	67.5	4.0	303	2	T21125	hypothetical prote
510	67.5	4.0	382	2	I48190	surface antigen -
511	67.5	4.0	450	2	T30970	hypothetical prote
512	67.5	4.0	478	2	H82185	6-phospho-beta-glu
513	67.5	4.0	483	2	F89364	protein F26D2.3 [l
514	67.5	4.0	494	1	B45738	alpha-amylase (EC
515	67.5	4.0	494	2	H91217	guanosine pentapho
516	67.5	4.0	494	2	A86064	hypothetical prote
517	67.5	4.0	544	2	S46099	hypothetical prote
518	67.5	4.0	554	2	G82272	DNA repair protein
519	67.5	4.0	637	2	B33785	myelin-associated
520	67.5	4.0	671	2	AF0042	probable oxidoredu
521	67.5	4.0	688	1	JC1469	beta-adrenergic-re
522	67.5	4.0	696	2	G81262	probable integral
523	67.5	4.0	809	2	T16448	hypothetical prote
524	67.5	4.0	860	2	F86349	hypothetical prote
525	67.5	4.0	905	2	S29329	hypothetical prote
526	67.5	4.0	1014	1	DEBY	oxoglutarate dehyd
527	67.5	4.0	1055	2	F64114	type I site-specif
528	67.5	4.0	1123	2	AD0865	exonuclease V chai
529	67.5	4.0	1451	2	T16388	hypothetical prote
530	67.5	4.0	1477	2	T18534	hypothetical prote
531	67.5	4.0	1570	2	AC2012	hypothetical prote
532	67.5	4.0	1753	2	S30855	hypothetical prote
533	67.5	4.0	1792	2	T08878	supervillin P205 -
534	67.5	4.0	1895	2	S50240	1,3-beta-glucan sy
535	67.5	4.0	1932	2	S53409	probable membrane
536	67.5	4.0	1951	2	B43963	RNA viral polymera
537	67.5	4.0	2227	1	GNNYMK	genome polyprotein
538	67.5	4.0	3898	1	GNNVHB	genome polyprotein
539	67.5	4.0	4063	2	T42993	probable spectrin
540	67.5	4.0	4101	2	T23630	hypothetical prote

541	67	4.0	163	2	F96569	hypothetical prote
542	67	4.0	283	2	H86547	hypothetical prote
543	67	4.0	283	2	G72075	hypothetical prote
544	67	4.0	303	2	D90684	recombination asso
545	67	4.0	303	2	H85534	hypothetical prote
546	67	4.0	303	2	S41303	yaId protein - Bgc
547	67	4.0	366	2	S53898	probable membrane
548	67	4.0	366	2	A71880	probable outer mem
549	67	4.0	367	2	T51455	auxin transport pr
550	67	4.0	386	2	F83958	succinyl-CoA synth
551	67	4.0	451	2	T40736	probable pseudouri
552	67	4.0	457	2	E71614	membrane transport
553	67	4.0	481	2	AE2327	hypothetical prote
554	67	4.0	483	2	AC1811	O-succinylbenzoyl-
555	67	4.0	493	2	T10054	pyruvate kinase (B
556	67	4.0	519	1	A54549	glucan 1,4-alpha-g
557	67	4.0	532	2	E84657	hypothetical prote
558	67	4.0	534	2	A83420	membrane-bound lyc
559	67	4.0	538	1	VGNZMM	cell fusion glycop
560	67	4.0	556	2	T51501	hypothetical prote
561	67	4.0	574	2	T08434	misato protein - f
562	67	4.0	576	2	T46385	hypothetical prote
563	67	4.0	583	2	T10051	pyruvate kinase (B
564	67	4.0	597	2	T41062	hypothetical prote
565	67	4.0	600	2	B84948	NADH2 dehydrogenas
566	67	4.0	636	2	G96717	hypothetical prote
567	67	4.0	640	2	T19346	hypothetical prote
568	67	4.0	652	2	A84461	probable fimbryn l
569	67	4.0	653	2	B82306	probable lipoprote
570	67	4.0	654	2	B85802	hypothetical prote
571	67	4.0	654	2	F90953	hypothetical prote
572	67	4.0	658	2	T46984	sensory transducer
573	67	4.0	658	2	AB0241	hypothetical prote
574	67	4.0	662	2	C91209	hypothetical prote
575	67	4.0	662	2	E86055	hypothetical prote
576	67	4.0	667	2	S66017	formate dehydrogen
577	67	4.0	675	2	B96542	unknown protein [l
578	67	4.0	691	2	T32748	hypothetical prote
579	67	4.0	781	2	AI3014	methyI-accepting c
580	67	4.0	788	2	F98269	hypothetical prote
581	67	4.0	810	2	T44430	protein PV100 [imp
582	67	4.0	1042	2	A57534	mucin 5AC (clone L
583	67	4.0	1139	2	B54962	sterol regulatory
584	67	4.0	1161	2	B86368	protein F28C11.9 [
586	67	4.0	1173	2	S48877	Ca2+-transporting
587	67	4.0	1309	2	F96509	protein F27F5.19 [
588	67	4.0	1464	1	S29159	glutamate receptor
589	67	4.0	1517	1	F65112	glutamate synthase
590	67	4.0	1518	2	C91140	glutamate synthase
591	67	4.0	1569	2	G02757	protein F2K11.14 [
592	67	4.0	1577	2	T15851	clathrin heavy cha
593	67	4.0	1640	2	T09522	hypothetical prote
594	67	4.0	1755	2	S69845	clathrin heavy cha
595	67	4.0	1755	2	S61763	TyB protein - yeas
596	67	4.0	1804	2	S56247	TyB protein - yeas
597	67	4.0	2278	1	S56274	probable membrane
598	67	4.0	2535	2	T04824	FAB1 protein - yea
599	67	4.0	3600	2	D86161	hypothetical prote
600	67	4.0	4351	2	T00252	Fl003.12 protein -
601	67	4.0	4563	1	LPHUB	MEGF1 protein - ra
602	66.5	3.9	186	2	C71601	apolipoprotein B-1
603	66.5	3.9	225	2	I67934	probable integral
604	66.5	3.9	239	1	Q4ECTD	neurofibromatosis
605	66.5	3.9	269	2	S04124	hypothetical 26.3K
606	66.5	3.9	275	2	T05595	kafirin precursor
607	66.5	3.9	282	2	S27769	hypothetical prote
608	66.5	3.9	296	2	T31062	NAD glycohydrolase
609	66.5	3.9	326	1	VGXRH4	hypothetical prote
610	66.5	3.9	357	2	A71938	glycoprotein VP7 p
611	66.5	3.9	362	2	T29552	probable proline p
612	66.5	3.9	378	1	S17412	hypothetical prote
613	66.5	3.9	380	2	S33720	ubiquinol-cytochro
						NS1 protein - deng
614	66.5	3.9	406	2	AE2455	hypothetical prote
615	66.5	3.9	408	2	H84825	hypothetical prote
616	66.5	3.9	431	2	T47528	hypothetical prote
617	66.5	3.9	431	2	B96671	hypothetical prote
618	66.5	3.9	448	2	T39314	hypothetical prote
619	66.5	3.9	472	2	S39507	glucuronosyl trans
620	66.5	3.9	474	2	T47957	tubulin gamma-1 ch
621	66.5	3.9	478	2	T33735	hypothetical prote
622	66.5	3.9	483	2	T39839	hypothetical prote
623	66.5	3.9	491	2	F87793	protein C27A12.6 [
624	66.5	3.9	524	2	S33640	homeotic protein s
625	66.5	3.9	537	1	JQ1619	cell fusion glycop
626	66.5	3.9	633	2	H96748	unknown protein T1
627	66.5	3.9	676	2	B47222	Kallmann syndrome
628	66.5	3.9	714	2	S66699	hypothetical prote
629	66.5	3.9	772	2	B82888	phenylalanine-tRNA
630	66.5	3.9	787	2	S47245	ActA protein - lis
631	66.5	3.9	805	2	T21957	hypothetical prote
632	66.5	3.9	821	2	AI2417	hypothetical prote
633	66.5	3.9	846	2	T38840	hypothetical trp-a
634	66.5	3.9	878	2	F64425	hypothetical trp-a
635	66.5	3.9	890	2	G64740	valine-tRNA ligase
636	66.5	3.9	890	2	A85501	[protein-Pil] urid
637	66.5	3.9	890	2	A90650	protein Pil-uridyI
638	66.5	3.9	928	2	T24868	hypothetical prote
639	66.5	3.9	1014	2	T17275	hypothetical prote
640	66.5	3.9	1047	2	B71402	hypothetical prote
641	66.5	3.9	1199	2	T18348	probable pol polyp
642	66.5	3.9	1426	2	T00337	hypothetical prote
643	66.5	3.9	1452	1	VGIH79	E2 glycoprotein pr
644	66.5	3.9	1502	1	RGBYH1	CYC1/CYP3 transcri
645	66.5	3.9	1755	2	S57045	TYB protein - yeas
646	66.5	3.9	1977	2	S54771	sodium channel alp
647	66.5	3.9	2109	1	ZLVN	genome polyprotein
648	66.5	3.9	2262	2	S16664	large protein l -
649	66.5	3.9	2297	2	AB2494	hypothetical prote
650	66.5	3.9	2311	1	TVCHSR	kinase-related pro
651	66.5	3.9	2325	2	A61208	chondroitin sulfat
652	66.5	3.9	2351	2	G71415	hypothetical prote
653	66.5	3.9	2894	2	C64474	genome polyprotein
654	66.5	3.9	3898	1	GNMVHC	dynein heavy chain
655	66.5	3.9	4639	1	A54794	hypothetical prote
656	66.5	3.9	183	2	T28711	competence negativ
657	66	3.9	217	2	AB1719	nonstructural prot
658	66	3.9	258	2	B49597	chitinase (EC 3.2.
659	66	3.9	266	2	T14345	porphobilinogen de
660	66	3.9	308	2	D89950	transcription fact
661	66	3.9	339	2	JC1442	protein gp41 - Org
662	66	3.9	367	2	T10352	hypothetical prote
663	66	3.9	373	2	D89865	protein R09F10.7 [
664	66	3.9	378	2	B89588	hypothetical prote
665	66	3.9	379	2	B70777	hypothetical prote
666	66	3.9	392	2	F81676	heat shock gene re
667	66	3.9	412	2	I46421	thyroxine-binding
668	66	3.9	414	2	AF0389	exonuclease Sbcd [
669	66	3.9	421	2	B90741	hypothetical prote
670	66	3.9	421	2	E85591	hypothetical prote
671	66	3.9	422	2	C83869	hypothetical prote
672	66	3.9	427	2	AI2148	processing protein
673	66	3.9	447	1	A42500	alpha-1,3-mannosyl
674	66	3.9	459	2	G71619	PiNT domain protei
675	66	3.9	532	2	T05942	cytochrome P450 82
676	66	3.9	566	2	S39732	arginine/ornithine
677	66	3.9	584	2	S55106	probable membrane
678	66	3.9	595	2	T41042	hypothetical prote
679	66	3.9	598	2	AG0311	NADH2 dehydrogenas
680	66	3.9	610	1	I46001	Cab-binding protei
681	66	3.9	638	1	YSBST2	threonine-tRNA lig
682	66	3.9	647	2	AG2114	hypothetical prote
683	66	3.9	679	2	B96599	protein F20N2.12 [
684	66	3.9	700	2	B84125	iron-sulphur-bindi
685	66	3.9	754	2	D88734	protein F32E10.1 [
686	66	3.9	779	2	B81287	hypothetical prote

687	66	3.9	779	2	S36111
688	66	3.9	795	2	E86247
689	66	3.9	840	2	A27832
690	66	3.9	858	2	T08881
691	66	3.9	913	2	T46339
692	66	3.9	921	2	F81294
693	66	3.9	927	2	T21772
694	66	3.9	937	2	A45082
695	66	3.9	1012	2	T13712
696	66	3.9	1026	2	T05882
697	66	3.9	1072	2	T37876
698	66	3.9	1102	2	T12681
699	66	3.9	1144	2	T13749
700	66	3.9	1172	2	S51623
701	66	3.9	1215	2	A86595
702	66	3.9	1215	2	B72029
703	66	3.9	1252	2	T00263
704	66	3.9	1260	1	TVRTNU
705	66	3.9	1348	2	B23496
706	66	3.9	1384	2	T18366
707	66	3.9	1397	2	T18377
708	66	3.9	1399	2	T18370
709	66	3.9	1412	2	T18380
710	66	3.9	1436	2	A46496
711	66	3.9	1450	2	T18382
712	66	3.9	1463	2	T18386
713	66	3.9	1465	2	T18384
714	66	3.9	1478	2	T18388
715	66	3.9	1503	2	T18389
716	66	3.9	1510	2	C84727
717	66	3.9	1512	2	T18392
718	66	3.9	1517	2	F85985
719	66	3.9	1538	2	AF0432
720	66	3.9	1571	2	T18395
721	66	3.9	1580	2	T18407
722	66	3.9	1770	2	S58651
723	66	3.9	1770	2	S70233
724	66	3.9	1770	2	S69948
725	66	3.9	1770	2	S69966
726	66	3.9	1770	2	S69950
727	66	3.9	1770	2	S70230
728	66	3.9	1771	2	S53592
729	66	3.9	2549	2	S45340
730	66	3.9	2549	2	A54837
731	66	3.9	2818	2	B55282
732	66	3.9	3898	2	S57437
733	66	3.9	3898	2	S58295
734	66	3.9	169	2	T06062
735	65.5	3.9	235	2	A97461
736	65.5	3.9	235	2	AC2679
737	65.5	3.9	250	2	T02392
738	65.5	3.9	262	2	C83970
739	65.5	3.9	262	2	D88930
740	65.5	3.9	268	2	T15169
741	65.5	3.9	319	2	H86218
742	65.5	3.9	319	2	JC4926
743	65.5	3.9	324	2	T28331
744	65.5	3.9	334	2	B84432
745	65.5	3.9	336	2	S52691
746	65.5	3.9	376	2	S27976
747	65.5	3.9	398	2	T02484
748	65.5	3.9	417	2	AB1528
749	65.5	3.9	422	2	T39893
750	65.5	3.9	429	2	F84015
751	65.5	3.9	433	2	T39745
752	65.5	3.9	435	2	E86515
753	65.5	3.9	435	2	C72107
754	65.5	3.9	436	2	A70923
755	65.5	3.9	437	2	A31142
756	65.5	3.9	439	2	G75314
757	65.5	3.9	452	2	G97826
758	65.5	3.9	452	2	F71672
759	65.5	3.9	462	2	S10235

osteoblast-specifi
receptor-like prot
cell division cont
prominin - mouse
hypothetical prote
probable helicase
hypothetical prote
neurotrophic recep
dof protein - frui
hypothetical prote
probable (Xeroderm
hypothetical prote
dof protein - frui
cut14 protein - fi
SWI/SNF family hel
helicase, Snf2/Rad
hypothetical prote
protein-tyrosine k
TyB protein - yeas
latrophilin-2, spl
latrophilin-2 (spl
latrophilin-2 (spl
latrophilin-2 (spl
antigen WCL.1 prec
latrophilin-2 (spl
latrophilin-2 (spl
latrophilin-2 (spl
latrophilin-3, spl
probable glucan sy
latrophilin-3, spl
glutamate synthase
glutamate synthase
latrophilin-3, spl
latrophilin-3, spl
TyB protein - yeas
TyB protein - yeas
TyB protein - yeas
TyB protein - yeas
TyB protein - yeas
TyB protein - yeas
TyB protein - yeas
FKBP-rapamycin-
rapamycin/FKBP12 t
neurofibromatosis-
genome polyprotein
polyprotein - hog
hypothetical prote
glutathione S-tran
glutathione S-tran
hypothetical prote
cell-division init
protein R1lg1.10
hypothetical prote
protein F22013.12
Xm1 endonuclease
ORF MSV170 hypothe
hypothetical prote
probable membrane
H+-transporting tw
hypothetical prote
sugar ABC transpor
probable signal tr
maltose/maltodextr
hypothetical prote
oligopeptide bindi
peptide ABC transp
hypothetical prote
gelsolin, ovarian
preprotein translo
cell division prot
cell division prot
alpha-L-fucosidase

760	65.5	3.9	468	2	T33784
761	65.5	3.9	470	2	B65175
762	65.5	3.9	495	2	F82123
763	65.5	3.9	526	2	T41944
764	65.5	3.9	528	2	F70218
765	65.5	3.9	552	2	A41035
766	65.5	3.9	553	2	T01416
767	65.5	3.9	558	2	A43667
768	65.5	3.9	584	2	E97303
769	65.5	3.9	589	2	A71277
770	65.5	3.9	589	2	G69815
771	65.5	3.9	609	2	A96693
772	65.5	3.9	619	2	B90141
773	65.5	3.9	653	2	B86184
774	65.5	3.9	669	2	T16626
775	65.5	3.9	684	2	T37944
776	65.5	3.9	745	2	I57665
777	65.5	3.9	752	2	G02273
778	65.5	3.9	757	2	T34351
779	65.5	3.9	772	2	A41860
780	65.5	3.9	784	2	T45697
781	65.5	3.9	792	2	T26050
782	65.5	3.9	794	2	S59069
783	65.5	3.9	906	2	G70767
784	65.5	3.9	954	2	S46177
785	65.5	3.9	985	2	A96777
786	65.5	3.9	994	1	TQECT5
787	65.5	3.9	1009	2	T42925
788	65.5	3.9	1014	2	S32613
789	65.5	3.9	1017	2	S67804
790	65.5	3.9	1061	2	JC7116
791	65.5	3.9	1078	2	T30879
792	65.5	3.9	1081	2	JC5494
793	65.5	3.9	1086	2	AF1662
794	65.5	3.9	1090	2	T30576
795	65.5	3.9	1139	2	S40932
796	65.5	3.9	1200	2	T48194
797	65.5	3.9	1217	1	EGMSMG
798	65.5	3.9	1224	2	T00059
799	65.5	3.9	1268	2	G85154
800	65.5	3.9	1303	2	E96805
801	65.5	3.9	1326	2	B56395
802	65.5	3.9	1449	1	A43573
803	65.5	3.9	1454	2	E84535
804	65.5	3.9	1465	2	A56395
805	65.5	3.9	1576	2	T21172
806	65.5	3.9	1584	2	T22674
807	65.5	3.9	1646	2	T20740
808	65.5	3.9	1974	2	T16703
809	65.5	3.9	2338	2	I73957
810	65.5	3.9	2555	2	C69681
811	65.5	3.9	2561	1	I40456
812	65.5	3.9	3388	2	T19997
813	65.5	3.9	3944	2	AH2515
814	65.5	3.9	4725	1	A44357
815	65.5	3.9	4936	2	D88040
816	65	3.8	169	2	S78046
817	65	3.8	189	2	F70574
818	65	3.8	219	2	T21495
819	65	3.8	234	2	TQ1695
820	65	3.8	239	2	AF1611
821	65	3.8	243	2	T16792
822	65	3.8	298	2	S75872
823	65	3.8	314	2	AC0464
824	65	3.8	317	2	T12333
825	65	3.8	344	2	A42053
826	65	3.8	356	1	F69798
827	65	3.8	361	2	C81960
828	65	3.8	375	2	T34015
829	65	3.8	381	2	T23915
830	65	3.8	387	2	A86032
831	65	3.8	393	2	S47789
832	65	3.8	393	2	

hypothetical prote
6-phospho-beta-glu
probable flagellar
hypothetical prote
GMP synthase (glut
chitinase (EC 3.2.
secy protein homol
serine C-palmitoyl
ABC-type multidrug
arginine-tRNA liga
ABC transporter (A
probable receptor
hypothetical prote
hypothetical prote
hypothetical prote
Sertoli cell leuci
LIV-1 protein - hu
hypothetical prote
tetracycline resis
hypothetical prote
hypothetical prote
z13 protein - mous
probable helicase
glucan 1,4-alpha-g
hypothetical prote
transposase - Esch
DNA-directed DNA p
HEX2 protein - yea
LRG1 protein - yea
Xsa1-3 protein - A
dynein heavy chain
protein-tyrosine k
cellulobiose-phospho
glucan synthase -
hypothetical prote
hypothetical prote
epidermal growth f
hypothetical prote
hypothetical prote
hypothetical prote
kinase-related pro
peptide synthetase
genome polyprotein
hypothetical prote
dynein heavy chain
hypothetical prote
protein F47F6.4 [I
ribonuclease 6 (EC
hypothetical prote
hypothetical prote
pathogenesis-relat
3-ketoacyl-acyl ca
hypothetical prote
hypothetical prote
cell division prot
NADH2 dehydrogenas
gap junction prote
conserved hypothet
hypothetical prote
hypothetical prote
xylose transport p
xylose transport p

833	65	3.8	393	2	C91185	xylose transport p	906	64.5	3.8	416	2	A56486	perinuclear bindin
834	65	3.8	393	2	T04957	hypothetical prote	907	64.5	3.8	424	2	T31862	hypothetical prote
835	65	3.8	399	1	S73883	yeife protein homol	908	64.5	3.8	439	2	T36472	probable DEAD-box
836	65	3.8	402	2	T40066	probable vacuolar	909	64.5	3.8	456	2	F84472	probable replicati
837	65	3.8	411	2	T29475	hypothetical prote	910	64.5	3.8	458	2	C87620	cytochrome P450 fa
838	65	3.8	433	2	H86178	hypothetical prote	911	64.5	3.8	477	2	A47236	zinc-finger protei
839	65	3.8	435	2	D72023	protoporphyrinogen	912	64.5	3.8	482	2	AB1421	beta-glucosidase h
840	65	3.8	440	2	A43519	complement recepto	913	64.5	3.8	490	2	T15097	hypothetical prote
841	65	3.8	467	2	S16915	gamma-aminobutyric	914	64.5	3.8	494	2	A48285	exopolysphatase
842	65	3.8	467	2	S19317	gamma-aminobutyric	915	64.5	3.8	516	2	B81684	exodeoxyribonuclea
843	65	3.8	469	2	D86144	protein probable U	916	64.5	3.8	522	2	H84671	hypothetical prote
844	65	3.8	475	2	T08753	hypothetical prote	917	64.5	3.8	523	2	T26740	hypothetical prote
845	65	3.8	479	2	F70965	hypothetical prote	918	64.5	3.8	534	2	G97703	hypothetical prote
846	65	3.8	480	2	A31589	carboxypeptidase C	919	64.5	3.8	551	2	T15127	hypothetical prote
847	65	3.8	497	2	JC5076	myc-associated zin	920	64.5	3.8	554	2	T28062	hypothetical prote
848	65	3.8	508	2	S74977	hypothetical prote	921	64.5	3.8	558	2	S57953	C4BP protein alpha
849	65	3.8	528	2	B42560	4-chlorobenzoate-C	922	64.5	3.8	584	2	T09113	response regulator
850	65	3.8	530	2	G02091	pancreatic zymogen	923	64.5	3.8	618	2	S33044	hypothetical prote
851	65	3.8	535	2	E87656	hypothetical prote	924	64.5	3.8	628	1	BWBSGA	glucose-inhibited
852	65	3.8	561	2	S62788	carboxylesterase (925	64.5	3.8	632	2	C70386	dnak-type molecula
853	65	3.8	578	2	B71431	hypothetical prote	926	64.5	3.8	636	2	A84903	hypothetical prote
854	65	3.8	592	2	S51371	transforming growt	927	64.5	3.8	640	2	T08758	hypothetical prote
855	65	3.8	613	2	T28952	hypothetical prote	928	64.5	3.8	667	2	B97012	methy1-accepting c
856	65	3.8	697	2	H86457	78.1K hypothetical	929	64.5	3.8	674	2	T23235	hypothetical prote
857	65	3.8	705	2	S55420	conserved hypothet	930	64.5	3.8	692	2	B86695	exclnuclease ABC s
858	65	3.8	809	2	S33533	heat shock protein	931	64.5	3.8	704	1	S33704	transforming prote
859	65	3.8	810	2	T33323	hypothetical prote	932	64.5	3.8	725	2	T17732	helicase-like prot
860	65	3.8	818	2	S64251	SAP4 protein - yea	933	64.5	3.8	734	2	T13674	hypothetical prote
861	65	3.8	836	2	D82177	conserved hypothet	934	64.5	3.8	743	2	T13673	hypothetical prote
862	65	3.8	856	2	A44439	protein kinase (EC	935	64.5	3.8	774	2	F96639	probable adenylate
863	65	3.8	880	2	T25358	regulatory protein	936	64.5	3.8	829	2	D71485	hypothetical prote
864	65	3.8	887	2	B84659	hypothetical prote	937	64.5	3.8	832	2	T31792	hypothetical prote
865	65	3.8	976	2	B84659	probable receptor-	938	64.5	3.8	838	2	D71492	hypothetical prote
866	65	3.8	1048	1	BVECSC	exonuclease (EC 3.	939	64.5	3.8	888	2	T51593	GTP-binding regula
867	65	3.8	1091	2	C95133	second chain of ma	940	64.5	3.8	901	1	FAHUA3	alpha-actinin 3 -
868	65	3.8	1091	2	G98001	hypothetical prote	941	64.5	3.8	901	2	T01135	probable GTP-bindi
869	65	3.8	1111	2	G96693	disease resistance	942	64.5	3.8	913	1	VGBEPS	glycoprotein gII p
870	65	3.8	1189	2	T52346	E2 glycoprotein pr	943	64.5	3.8	935	2	S57080	hypothetical prote
871	65	3.8	1225	1	S24284	adenylate cyclase	944	64.5	3.8	938	2	T01809	hypothetical prote
872	65	3.8	1248	2	A53588	hypothetical prote	945	64.5	3.8	973	2	JQ0971	transposase tnpA -
873	65	3.8	1253	2	T21065	hypothetical prote	946	64.5	3.8	980	1	TVCTMD	macrophage colony-
874	65	3.8	1320	2	F96614	probable copia-tyr	947	64.5	3.8	1031	2	C81302	probable type I si
875	65	3.8	1321	2	T23476	hypothetical prote	948	64.5	3.8	1052	1	A44937	kinetoplast-associ
876	65	3.8	1321	2	S27337	multidrug resistan	949	64.5	3.8	1052	2	A46166	protein-tyrosine k
877	65	3.8	1372	2	S18921	genome polyprotein	950	64.5	3.8	1124	2	JH0588	calmodulin-binding
878	65	3.8	1616	2	G64242	cytadherence-acces	951	64.5	3.8	1265	2	F71429	hypothetical prote
879	65	3.8	1744	2	JH0720	tanabin - African	952	64.5	3.8	1350	2	T30341	zinc finger protei
880	65	3.8	2077	2	T43991	large tegument pro	953	64.5	3.8	1531	2	T42218	sItc-1 protein hom
881	65	3.8	2098	2	T25888	hypothetical prote	954	64.5	3.8	1616	2	S62504	conserved hypothet
882	65	3.8	2133	2	T30637	hypothetical prote	955	64.5	3.8	1755	2	S69963	TYB protein - yeas
883	65	3.8	2253	2	T30336	nuclear/mitotic ap	956	64.5	3.8	1755	2	S69839	TYB protein - yeas
884	65	3.8	2354	2	T13288	mei-41 protein - f	957	64.5	3.8	1755	2	S69980	TYB protein - yeas
885	65	3.8	4543	1	A53102	alpha-2-macroglobu	958	64.5	3.8	2139	2	A35672	crumbs protein - f
886	64.5	3.8	159	2	T10363	hypothetical prote	959	64.5	3.8	2194	1	JQ1977	glutamate synthase
887	64.5	3.8	170	2	S67318	hypothetical prote	960	64.5	3.8	2227	1	GNNYHM	genome polyprotein
888	64.5	3.8	176	2	A99136	hypothetical prote	961	64.5	3.8	2234	2	S32920	cell wall-associat
889	64.5	3.8	176	2	AB3152	hypothetical prote	962	64.5	3.8	3449	2	T01083	hypothetical prote
890	64.5	3.8	197	2	T21030	outer membrane lip	963	64.5	3.8	3766	2	T29165	hypothetical prote
891	64.5	3.8	216	1	S58576	hypothetical prote	964	64.5	3.8	140	2	F64490	ADP-ribosylation f
892	64.5	3.8	245	2	A41858	hypothetical prote	965	64	3.8	179	2	JH0260	hypothetical prote
893	64.5	3.8	272	2	B90544	hypothetical prote	966	64	3.8	246	2	T00541	hypothetical prote
894	64.5	3.8	275	2	T28738	hypothetical prote	967	64	3.8	260	2	A55122	hypothetical prote
895	64.5	3.8	285	2	T29490	hypothetical prote	968	64	3.8	263	2	A82069	deoxycytidine kina
896	64.5	3.8	322	2	T02270	hypothetical prote	969	64	3.8	265	2	T14348	hypothetical prote
897	64.5	3.8	326	2	T08849	alternative respir	970	64	3.8	326	1	JQ1444	probable chitinase
898	64.5	3.8	331	2	B47236	zinc-finger protei	971	64	3.8	326	1	VGXR37	glycoprotein VP7 p
899	64.5	3.8	336	1	WMVZP1	F1 protein - fowlp	972	64	3.8	340	2	A83332	anthranilate dioxy
900	64.5	3.8	371	2	S32604	collagen alpha 2(V	973	64	3.8	352	2	T05106	connexin40 - human
901	64.5	3.8	374	2	T02315	hypothetical prote	974	64	3.8	358	2	T38429	hypothetical prote
902	64.5	3.8	386	1	JH0610	acid phosphatase (975	64	3.8	361	2	G89916	hypothetical prote
903	64.5	3.8	390	2	A86065	UDP-N-acetyl gluco	976	64	3.8	389	2	B81380	hypothetical prote
904	64.5	3.8	390	2	G91218	UDP-N-acetyl gluco	977	64	3.8	395	2	H96513	hypothetical prote
905	64.5	3.8	397	2	C84904	hypothetical prote	978	64	3.8	418	2	S29506	neurotensin recept

979	64	3.8	418	2	T25092	hypothetical prote	1052	63.5	3.7	188	2	D69652	transcription repr
980	64	3.8	447	2	JC7153	phosphoprotein pho	1053	63.5	3.7	189	2	AB0560	conserved hypothet
981	64	3.8	447	2	S65686	protein phosphatas	1054	63.5	3.7	190	2	G85542	glycoprotein/polys
982	64	3.8	452	2	A55836	phosphoprotein pho	1055	63.5	3.7	190	2	C90692	glycoprotein/polys
983	64	3.8	452	2	C85024	probable polygalac	1056	63.5	3.7	190	2	E64775	probable lipoprote
984	64	3.8	467	2	A71431	hypothetical prote	1057	63.5	3.7	199	2	JS0430	prolactin - elepha
985	64	3.8	468	2	T25475	hypothetical prote	1058	63.5	3.7	215	2	S64690	a2-mating type pro
986	64	3.8	472	2	A33312	sarcoplasmic retic	1059	63.5	3.7	216	2	C90956	probable membrane
987	64	3.8	472	2	H96607	unknown protein F2	1060	63.5	3.7	216	2	H85804	unknown protein en
988	64	3.8	474	1	OMHTUB	alpha-1-B-glycopro	1061	63.5	3.7	217	2	AH0561	potential acrAB op
989	64	3.8	483	2	T40801	hypothetical prote	1062	63.5	3.7	228	2	H83867	hypothetical prote
990	64	3.8	492	2	T02458	hypothetical prote	1063	63.5	3.7	246	2	C96780	thaumatin-like pro
991	64	3.8	504	2	T50270	hypothetical prote	1064	63.5	3.7	260	2	AF0915	probable deoxyribo
992	64	3.8	507	1	A30828	steroid 17alpha-mo	1065	63.5	3.7	262	2	G02476	lysosomal-associat
993	64	3.8	523	2	AS3196	orphan hormone nuc	1066	63.5	3.7	285	2	T22616	hypothetical prote
994	64	3.8	525	2	A70157	hypothetical prote	1067	63.5	3.7	305	2	E84848	probable RING zinc
995	64	3.8	527	2	T01019	transport protein	1068	63.5	3.7	312	2	AH2389	hypothetical prote
996	64	3.8	572	2	F96755	hypothetical prote	1069	63.5	3.7	315	2	T47181	hypothetical prote
997	64	3.8	594	2	A49804	cellular Hsp70 hom	1070	63.5	3.7	326	1	VGXRAB	glycoprotein VP7 p
998	64	3.8	598	2	T25207	hypothetical prote	1071	63.5	3.7	351	2	T29369	hypothetical prote
999	64	3.8	604	2	T37870	RNA-binding / Ran	1072	63.5	3.7	355	2	AF0454	uoporphyrinogen d
1000	64	3.8	605	2	T31690	hypothetical prote	1073	63.5	3.7	366	2	JC7690	Gfi-1-like protein
1001	64	3.8	620	2	AF2174	hypothetical prote	1074	63.5	3.7	369	2	F87422	hypothetical prote
1002	64	3.8	630	2	D86391	TiK7.17 protein -	1075	63.5	3.7	369	2	T40279	hypothetical prote
1003	64	3.8	632	2	T00108	hypothetical prote	1076	63.5	3.7	370	2	H90675	probable ATP bindi
1004	64	3.8	643	2	S36017	finger protein tra	1077	63.5	3.7	371	2	AF2396	two-component sens
1005	64	3.8	648	2	S16866	gene H19 protein -	1078	63.5	3.7	373	2	B39732	H+-transporting tw
1006	64	3.8	651	2	F64457	methionine-tRNA li	1079	63.5	3.7	379	2	T24814	hypothetical prote
1007	64	3.8	654	1	ORECCS	chemotaxis protein	1080	63.5	3.7	383	2	T39854	hypothetical prote
1008	64	3.8	655	2	A57681	hypothetical prote	1081	63.5	3.7	388	2	T31887	hypothetical prote
1009	64	3.8	716	2	G82627	hypothetical prote	1082	63.5	3.7	388	2	A88949	protein R09B5.5 [i
1010	64	3.8	767	2	T41344	probable zinc-fing	1083	63.5	3.7	388	2	T31888	hypothetical prote
1011	64	3.8	769	2	S55554	male-specific leth	1084	63.5	3.7	392	2	C85526	hypothetical prote
1012	64	3.8	773	2	T39513	hypothetical prote	1085	63.5	3.7	395	2	A48641	hypothetical prote
1013	64	3.8	774	2	JC7265	neprilysin (EC 3.4	1086	63.5	3.7	396	2	T22097	hypothetical prote
1014	64	3.8	794	2	T46073	hypothetical prote	1087	63.5	3.7	398	2	S77230	hypothetical prote
1015	64	3.8	808	2	T22363	hypothetical prote	1088	63.5	3.7	398	2	T19421	hypothetical prote
1016	64	3.8	820	2	G86246	hypothetical prote	1089	63.5	3.7	404	2	E82012	hypothetical prote
1017	64	3.8	857	2	T04208	probable anthranil	1090	63.5	3.7	404	2	F81240	sodium/glutamate s
1018	64	3.8	908	2	A33280	sarcalumenin precu	1091	63.5	3.7	420	2	F83494	hypothetical prote
1019	64	3.8	916	2	F71962	hypothetical prote	1092	63.5	3.7	432	2	T20536	hypothetical prote
1020	64	3.8	931	2	A49737	dipeptidyl aminope	1093	63.5	3.7	434	2	T20539	hypothetical prote
1021	64	3.8	937	2	T41400	probable peroxisom	1094	63.5	3.7	435	2	T43749	cytochrome oxidase
1022	64	3.8	976	2	URRTAP	peptidylglycine mo	1095	63.5	3.7	439	2	T28196	hypothetical prote
1023	64	3.8	976	1	PC4208	valine-cRNA ligase	1096	63.5	3.7	459	2	A34791	hypothetical prote
1024	64	3.8	987	2	A54092	protein-tyrosine k	1097	63.5	3.7	459	2	A75097	interleukin-7 rece
1025	64	3.8	1002	2	B54145	sodium-chloride tr	1098	63.5	3.7	463	2	F81194	hypothetical prote
1026	64	3.8	1008	2	T04462	hypothetical prote	1099	63.5	3.7	463	2	E81830	hypothetical prote
1027	64	3.8	1012	2	T41940	DNA polymerase - h	1100	63.5	3.7	468	2	S61964	probable membrane
1028	64	3.8	1017	2	G85055	probable polyprote	1101	63.5	3.7	470	2	S68964	legumin precursor
1029	64	3.8	1099	2	C72363	carbamoyl-phosphat	1102	63.5	3.7	474	2	H84210	hypothetical prote
1030	64	3.8	1133	1	S41478	DNA repair protein	1103	63.5	3.7	475	2	I38597	1-aminocyclopropan
1031	64	3.8	1146	2	F84487	probable ABC trans	1104	63.5	3.7	481	2	AB1890	type I serine-thre
1032	64	3.8	1242	2	T39453	probable mrna stab	1105	63.5	3.7	481	2	S74934	hypothetical prote
1033	64	3.8	1272	2	T49313	copia-type reverse	1106	63.5	3.7	488	2	D70614	lamin B2 - human
1034	64	3.8	1284	2	T50993	hypothetical prote	1107	63.5	3.7	491	2	T03978	probable protein
1035	64	3.8	1299	1	WMBEHS	membrane antigen P	1108	63.5	3.7	505	2	IS3417	ABC transporter, A
1036	64	3.8	1335	2	H75511	DNA polymerase III	1109	63.5	3.7	515	2	T25534	LZTR-1 - human
1037	64	3.8	1389	2	T41230	hypothetical TPR d	1110	63.5	3.7	514	2	A45023	cell fusion protei
1038	64	3.8	1455	2	E75199	DNA-directed DNA p	1111	63.5	3.7	539	2	C96758	hypothetical prote
1039	64	3.8	1518	2	T28880	hypothetical prote	1112	63.5	3.7	546	1	C70393	beta-glucosidase h
1040	64	3.8	1588	2	T38660	probable transcrip	1113	63.5	3.7	547	2	E81017	hypothetical prote
1041	64	3.8	1672	2	T46237	hypothetical prote	1114	63.5	3.7	552	2	I54388	thymidine kinase (
1042	64	3.8	1684	2	T02632	hypothetical prote	1115	63.5	3.7	572	1	VGNZBA	centromere protein
1043	64	3.8	1733	2	D70887	probable polyketid	1116	63.5	3.7	574	2	JQ1583	ABC transporter pe
1044	64	3.8	1756	2	S45867	TyB protein - yeas	1117	63.5	3.7	575	2	D96585	hypothetical prote
1045	64	3.8	1783	2	T37258	probable voltage-d	1118	63.5	3.7	575	2	G69834	transporter bindin
1046	64	3.8	1917	2	C88728	protein C48A7.1 [i	1119	63.5	3.7	591	2	T02402	hypothetical prote
1047	64	3.8	2121	2	A59233	myosin VII-like pr	1120	63.5	3.7	601	2	T24694	hypothetical prote
1048	64	3.8	2124	2	T01526	hypothetical prote	1121	63.5	3.7	607	1	KIBETE	hypothetical prote
1049	64	3.8	2261	1	A42548	genome polyprotein	1122	63.5	3.7	608	2	S51790	chymidine kinase (
1050	64	3.8	3119	2	T18414	protein g377 - mal	1123	63.5	3.7	633	2	G89836	hypothetical prote
1051	64	3.8	4273	2	C69679	polyketide synthas	1124	63.5	3.7	689	2	T25202	hypothetical prote

1125	63.5	3.7	693	2	F86156	hypothetical prote	1198	63	3.7	316	2	S35516	type II site-speci
1126	63.5	3.7	704	1	S25820	dynammin-related pr	1199	63	3.7	320	2	T19358	hypothetical prote
1127	63.5	3.7	706	1	Q0BE6L	glycoprotein H - h	1200	63	3.7	326	1	VGXRB7	glycoprotein VP7 p
1128	63.5	3.7	765	2	AD1656	cobalamin-Independ	1201	63	3.7	335	2	A39743	u-plasminogen acti
1129	63.5	3.7	799	2	S18209	fibroblast growth	1202	63	3.7	335	2	JC1441	transcription fact
1130	63.5	3.7	851	2	A59284	unconventional myo	1203	63	3.7	336	2	AH2040	porphobilinogen de
1131	63.5	3.7	858	2	AD2272	protein serine-thr	1204	63	3.7	336	2	T50560	SINAH1 protein [im
1132	63.5	3.7	882	2	F86164	hypothetical prote	1205	63	3.7	346	2	T48496	membrane protein -
1133	63.5	3.7	888	2	E71608	ATP-dept. acyl-CoA	1206	63	3.7	348	2	A41784	tumor necrosis fac
1134	63.5	3.7	903	2	T20804	hypothetical prote	1207	63	3.7	357	2	T03557	ribose transport s
1135	63.5	3.7	903	2	G87372	TonB-dependent rec	1208	63	3.7	358	2	C96036	probable ferredoxi
1136	63.5	3.7	922	2	T23573	hypothetical prote	1209	63	3.7	385	2	E86603	cell division prot
1137	63.5	3.7	926	2	S39344	deubiquinating enz	1210	63	3.7	385	2	B72022	2-hydroxyglutaryl-
1138	63.5	3.7	928	2	S40745	hypothetical prote	1211	63	3.7	391	2	E69494	protochlorophyllid
1139	63.5	3.7	935	2	T48778	hypothetical prote	1212	63	3.7	398	2	JC4146	hypothetical prote
1140	63.5	3.7	956	1	Q0BEK2	UL105 protein - hu	1213	63	3.7	403	2	T02290	hypothetical prote
1141	63.5	3.7	974	2	A90140	conserved hypothet	1214	63	3.7	405	2	T16836	hypothetical prote
1142	63.5	3.7	1011	2	T29806	hypothetical prote	1215	63	3.7	410	2	E85617	hypothetical prote
1143	63.5	3.7	1011	2	A12046	ABC transporter At	1216	63	3.7	410	2	G90753	hypothetical prote
1144	63.5	3.7	1029	1	S21369	collagen alpha 2(V	1217	63	3.7	416	2	A70110	conserved hypothet
1145	63.5	3.7	1036	2	F71565	probable isoleucin	1218	63	3.7	421	2	D81374	probable oxidoredu
1146	63.5	3.7	1061	2	D69799	cytochrome P450 /	1219	63	3.7	427	2	A53964	carboxyl-terminal
1147	63.5	3.7	1080	2	T43164	IactA protein - Li	1220	63	3.7	433	2	T08938	hypothetical prote
1148	63.5	3.7	1100	2	G84534	probable retroelem	1221	63	3.7	440	2	H95373	probable Nreb prot
1149	63.5	3.7	1122	2	S64443	probable membrane	1222	63	3.7	465	2	T00982	En/Spm-like transp
1150	63.5	3.7	1131	2	T07137	phytochrome A - so	1223	63	3.7	471	2	S46739	hypothetical prote
1151	63.5	3.7	1133	1	EGRT	epidermal growth f	1224	63	3.7	473	2	B84143	Na+/H+ antiporter
1152	63.5	3.7	1177	2	AD0438	probable exported	1225	63	3.7	476	2	T46067	hypothetical prote
1153	63.5	3.7	1328	2	S52481	TyB protein - yeas	1226	63	3.7	479	2	S52705	probable membrane
1154	63.5	3.7	1338	2	A49634	aldehyde oxidase (1227	63	3.7	482	2	T30983	hypothetical prote
1155	63.5	3.7	1391	2	S50608	hypothetical prote	1228	63	3.7	505	2	T50815	cdce2-like protein
1156	63.5	3.7	1418	2	T15232	hypothetical prote	1229	63	3.7	518	2	T50175	dna-directed rna p
1157	63.5	3.7	1463	2	A53210	phospholipase A2 r	1230	63	3.7	532	2	T47335	hypothetical prote
1158	63.5	3.7	1616	1	JQ2144	183K protein - tom	1231	63	3.7	533	2	AH2574	hypothetical prote
1159	63.5	3.7	1628	2	T43682	nucleoporin - f188	1232	63	3.7	555	2	F83949	probable Athila re
1160	63.5	3.7	1652	2	T16799	hypothetical prote	1233	63	3.7	555	2	H84476	hypothetical prote
1161	63.5	3.7	1661	2	T21986	hypothetical prote	1234	63	3.7	561	2	T34083	chitinase (EC 3.2.
1162	63.5	3.7	1663	2	T21993	hypothetical prote	1235	63	3.7	562	2	B41035	probable membrane
1163	63.5	3.7	1711	2	T21432	hypothetical prote	1236	63	3.7	586	2	S58713	hypothetical prote
1164	63.5	3.7	1751	2	T50002	hypothetical prote	1237	63	3.7	586	2	B83790	hypothetical prote
1165	63.5	3.7	1755	2	S69979	TyB protein - yeas	1238	63	3.7	590	2	T56526	interleukin 1 rece
1166	63.5	3.7	1755	2	S69975	TyB protein - yeas	1239	63	3.7	590	2	B84898	hypothetical prote
1167	63.5	3.7	1755	2	S50641	TyB protein YER138	1240	63	3.7	592	2	A42100	transforming growt
1168	63.5	3.7	1755	2	S69960	TyB protein - yeas	1241	63	3.7	622	2	T37257	hypothetical prote
1169	63.5	3.7	1957	2	S68453	sodium channel pro	1242	63	3.7	634	2	S31925	beta-fructofuranos
1170	63.5	3.7	2017	1	A36014	myosin heavy chain	1243	63	3.7	643	2	S70592	NADH2 dehydrogenas
1171	63.5	3.7	2057	2	S61477	myosin II heavy ch	1244	63	3.7	647	2	JB0337	Frizzled-1 protein
1172	63.5	3.7	2227	1	GNNYHR	genome polyprotein	1245	63	3.7	674	2	S18670	dnak-cytc molecula
1173	63.5	3.7	2340	2	I48310	kinase-related pro	1246	63	3.7	677	2	B82870	DNA topoisomerase
1174	63.5	3.7	2692	2	T23768	hypothetical prote	1247	63	3.7	686	2	JB5708	villin-like protei
1175	63.5	3.7	2783	1	A41948	alpha-fetoprotein	1248	63	3.7	710	2	T25734	hypothetical prote
1176	63.5	3.7	3570	2	T45025	mucin MUC5B, trach	1249	63	3.7	728	2	T20561	hypothetical prote
1177	63	3.7	111	2	S37202	Ig kappa chain V r	1250	63	3.7	738	2	T45916	hypothetical prote
1178	63	3.7	117	2	T14465	lipid transfer pro	1251	63	3.7	764	2	JC4736	methyl-accepting c
1179	63	3.7	158	2	F84776	probable RAV2-like	1252	63	3.7	767	2	S63220	probable membrane
1180	63	3.7	161	2	T41833	AcMNPV orf93 - Bom	1253	63	3.7	790	2	S27458	SMY2 protein - yea
1181	63	3.7	168	2	B71486	hypothetical prote	1254	63	3.7	851	2	A46160	interferon alpha-i
1182	63	3.7	175	2	S37649	high-sulfur kerati	1255	63	3.7	870	2	A96637	hypothetical prote
1183	63	3.7	197	2	S74851	hypothetical prote	1256	63	3.7	874	2	T15570	hypothetical prote
1184	63	3.7	204	1	WZVZB3	24K HindIII-C prot	1257	63	3.7	876	2	D70971	3', 5'-cyclic nucle
1185	63	3.7	204	2	I42503	CSL protein - vacc	1258	63	3.7	885	2	JC7898	gene boss protein
1186	63	3.7	207	2	B83523	hypothetical prote	1259	63	3.7	896	2	S26740	protein TIF9.20 [i
1187	63	3.7	215	2	D41681	S-crystallin 4 - g	1260	63	3.7	925	2	H96638	probable family 31
1188	63	3.7	227	2	H82449	hypothetical prote	1261	63	3.7	993	2	T38598	type III restricti
1189	63	3.7	249	2	S09868	hypothetical prote	1262	63	3.7	1001	2	H64593	glutamate receptor
1190	63	3.7	280	2	AC0411	probable priplasm	1263	63	3.7	1009	2	S28857	receptor-kinase li
1191	63	3.7	284	2	T25938	hypothetical prote	1264	63	3.7	1011	2	T45718	hypothetical prote
1192	63	3.7	295	2	AB1566	probable UDP-gluc	1265	63	3.7	1027	2	D64296	myosin-like protei
1193	63	3.7	297	2	F69145	hypothetical prote	1266	63	3.7	1054	2	D96519	acrosomal protein
1194	63	3.7	301	2	S20081	surface virulence	1267	63	3.7	1060	2	S63993	dynein heavy chain
1195	63	3.7	309	2	T27426	hypothetical prote	1268	63	3.7	1066	2	T30297	hypothetical prote
1196	63	3.7	309	2	T16660	crRNA delta(2)-isop	1269	63	3.7	1165	2	T21636	thrombospondin 2 p
1197	63	3.7	313	2	A81142		1270	63	3.7	1172	1	TSHUP2	

1271	63	3.7	1209	2	T16663	hypothetical prote
1272	63	3.7	1210	2	S35548	DNA-directed RNA p
1273	63	3.7	1286	1	H36845	DNA-directed RNA p
1274	63	3.7	1286	2	T28521	DNA-directed RNA p
1275	63	3.7	1286	2	A72161	M6R protein - vari
1276	63	3.7	1299	2	T43251	furin (EC 3.4.21.7
1277	63	3.7	1329	2	T33136	hypothetical prote
1278	63	3.7	1426	2	A99580	hypothetical prote
1279	63	3.7	1460	2	T00095	hypothetical prote
1280	63	3.7	1464	2	A43274	N-methyl D-asparta
1281	63	3.7	1486	2	A10906	glutamate synthase
1282	63	3.7	1513	2	A54895	mucin 2, intestina
1283	63	3.7	1535	2	S46224	peroxidasin - frui
1284	63	3.7	1624	2	T25592	hypothetical prote
1285	63	3.7	1642	2	T08880	NMDA receptor-bind
1286	63	3.7	1662	1	H71402	probable kinase -
1287	63	3.7	1818	1	S73852	hypothetical prote
1288	63	3.7	1839	1	RRWPEM	genome polypeptid
1289	63	3.7	2374	2	T21052	hypothetical prote
1290	63	3.7	2748	2	S57976	nuclear migration
1291	63	3.7	4544	1	S02392	alpha-2-macroglobu
1292	62.5	3.7	135	2	A13164	hypothetical prote
1293	62.5	3.7	151	2	A47667	VP5 homolog - bovi
1294	62.5	3.7	169	2	A25652	protein kinase (EC
1295	62.5	3.7	184	2	E71504	hypothetical prote
1296	62.5	3.7	206	2	H71531	superoxide dismuta
1297	62.5	3.7	225	2	F87528	hypothetical prote
1298	62.5	3.7	226	2	A64152	probable thiamine-
1299	62.5	3.7	235	2	S15655	zein, 19K - maize
1300	62.5	3.7	253	2	F89790	conserved hypothet
1301	62.5	3.7	259	2	H81159	conserved hypothet
1302	62.5	3.7	261	2	T11948	ycfl protein - red
1303	62.5	3.7	267	2	T02983	22K zein precursor
1304	62.5	3.7	269	2	B35678	enkephalin precurs
1305	62.5	3.7	270	2	E84578	probable senescenc
1306	62.5	3.7	274	2	T42648	hypothetical prote
1307	62.5	3.7	291	2	G97327	short-chain alcoh
1308	62.5	3.7	306	2	T19412	hypothetical prote
1309	62.5	3.7	323	2	E70190	ATP-binding protei
1310	62.5	3.7	328	2	E88930	protein R1G11.11
1311	62.5	3.7	332	2	G89152	protein C24B5.5 [l
1312	62.5	3.7	332	2	B85588	probable membrane
1313	62.5	3.7	332	2	A99738	hypothetical prote
1314	62.5	3.7	366	2	B84245	DNA topoisomerase
1315	62.5	3.7	371	2	G97321	alpha/beta superfa
1316	62.5	3.7	375	2	S50228	PAS7 protein - yea
1317	62.5	3.7	380	2	S77053	magnesium/cobalt t
1318	62.5	3.7	399	2	A10260	probable aminotran
1319	62.5	3.7	400	2	S58222	PQ-rich protein -
1320	62.5	3.7	401	2	AG1238	hypothetical prote
1321	62.5	3.7	407	2	AG2415	two-component hybr
1322	62.5	3.7	418	2	S49643	hypothetical prote
1323	62.5	3.7	419	2	T10652	hypothetical prote
1324	62.5	3.7	427	2	S41087	inward rectifier p
1325	62.5	3.7	427	2	S52846	potassium channel,
1326	62.5	3.7	453	2	S11087	gamma-aminobutyric
1327	62.5	3.7	475	2	A12439	hypothetical prote
1328	62.5	3.7	479	2	S73770	NADH oxidase nox -
1329	62.5	3.7	481	2	AE0911	Tltd protein limpo
1330	62.5	3.7	485	2	E72115	hypothetical prote
1331	62.5	3.7	488	2	T05313	hypothetical prote
1332	62.5	3.7	493	2	C71903	D-alanyl-D-alanine
1333	62.5	3.7	495	1	A45738	alpha-amyase (EC
1334	62.5	3.7	495	2	B85810	cytoplasmic alpha-
1335	62.5	3.7	495	2	B90962	cytochrome-c oxida
1336	62.5	3.7	508	2	S74200	hypothetical prote
1337	62.5	3.7	517	2	T07704	hypothetical prote
1338	62.5	3.7	519	2	T44269	probable photomorp
1339	62.5	3.7	532	2	F84901	lens fiber cell be
1340	62.5	3.7	533	2	TC1103	methyl-accepting c
1341	62.5	3.7	534	2	B69896	acetyl choline rec
1342	62.5	3.7	548	2	T23270	
1343	62.5	3.7				
1344	62.5	3.7	1344	2	A57189	secy protein homol
1345	62.5	3.7	1345	2	P84567	probable preprotei
1346	62.5	3.7	1346	2	T45137	phosphoprotein pho
1347	62.5	3.7	1347	2	T50310	phosphoprotein pho
1348	62.5	3.7	1348	2	P1WL18	L1 protein - human
1349	62.5	3.7	1349	1	VGNZR2	cell fusion glycop
1350	62.5	3.7	1350	1	VGNZA2	cell fusion glycop
1351	62.5	3.7	1351	1	VGNZBR	cell fusion glycop
1352	62.5	3.7	1352	2	B28929	cell fusion glycop
1353	62.5	3.7	1353	2	S37254	cell fusion protei
1354	62.5	3.7	1354	2	T38775	hypothetical prote
1355	62.5	3.7	1355	2	G86204	hypothetical prote
1356	62.5	3.7	1356	1	S11777	hydrogenase (EC 1.
1357	62.5	3.7	1357	2	T24315	hypothetical prote
1358	62.5	3.7	1358	1	A61084	myelin-associated
1359	62.5	3.7	1359	2	B98058	endopeptidase O (E
1360	62.5	3.7	1360	2	G01205	tyl protein - huma
1361	62.5	3.7	1361	2	T20046	hypothetical prote
1362	62.5	3.7	1362	2	T26835	hypothetical prote
1363	62.5	3.7	1363	2	A38436	mitosis initiation
1364	62.5	3.7	1364	2	A95144	hypothetical prote
1365	62.5	3.7	1365	2	G98011	hypothetical prote
1366	62.5	3.7	1366	2	T04774	hypothetical prote
1367	62.5	3.7	1367	2	T41357	anthranilate phosp
1368	62.5	3.7	1368	2	T49911	hypothetical prote
1369	62.5	3.7	1369	2	T01025	hypothetical prote
1370	62.5	3.7	1370	2	I64115	phenylalanine-tRNA
1371	62.5	3.7	1371	2	AH1302	primosomal replica
1372	62.5	3.7	1372	2	E83963	hypothetical prote
1373	62.5	3.7	1373	2	B70692	hypothetical prote
1374	62.5	3.7	1374	2	E70105	p15 protein homol
1375	62.5	3.7	1375	2	C96639	protein T1F9.14 [l
1376	62.5	3.7	1376	2	JC8051	protein tyrosine p
1377	62.5	3.7	1377	2	T20422	hypothetical prote
1378	62.5	3.7	1378	2	A36617	3',5'-cyclic-GMP p
1379	62.5	3.7	1379	2	A42828	protein ZC53.4 [lm
1380	62.5	3.7	1380	2	B89472	hypothetical prote
1381	62.5	3.7	1381	2	T49010	respiratory burst
1382	62.5	3.7	1382	2	F69552	leucyl-tRNA synthe
1383	62.5	3.7	1383	2	S76501	preprotein translo
1384	62.5	3.7	1384	2	T51137	ionotropic glutama
1385	62.5	3.7	1385	2	JC5527	bone morphogenetic
1386	62.5	3.7	1386	2	I53012	focal adhesion kin
1387	62.5	3.7	1387	2	S63252	hypothetical prote
1388	62.5	3.7	1388	2	S40908	TYB protein - yeas
1389	62.5	3.7	1389	2	T18312	hypothetical prote
1390	62.5	3.7	1390	2	B28097	TYB protein - yeas
1391	62.5	3.7	1391	2	T19691	hypothetical prote
1392	62.5	3.7	1392	2	B86292	F7H2.12 protein -
1393	62.5	3.7	1393	2	VGIHE3	E2 glycoprotein pr
1394	62.5	3.7	1394	1	VGIHE2	E2 glycoprotein pr
1395	62.5	3.7	1395	1	VGIHE2	E2 glycoprotein pr
1396	62.5	3.7	1396	2	S47423	E2 glycoprotein pr
1397	62.5	3.7	1397	2	S41453	spike protein - ca
1398	62.5	3.7	1398	2	T33318	hypothetical prote
1399	62.5	3.7	1399	2	T33318	hypothetical prote
1400	62.5	3.7	1400	2	J50703	DNA topoisomerase
1401	62.5	3.7	1401	2	T25808	hypothetical prote
1402	62.5	3.7	1402	2	T28923	sucrose alpha-gluc
1403	62.5	3.7	1403	1	UUHU	hypothetical prote
1404	62.5	3.7	1404	2	T49273	mcprd protein - mo
1405	62.5	3.7	1405	2	JW0059	cell wall-associat
1406	62.5	3.7	1406	2	AF1489	genome polypeptid
1407	62.5	3.7	1407	2	S47307	nonstructural poly
1408	62.5	3.7	1408	1	C44213	nonstructural poly
1409	62.5	3.7	1409	1	MNWVTD	toxin A - Clostrid
1410	62.5	3.7	1410	2	A37052	giant protein p619
1411	62.5	3.7	1411	2	S71752	hypothetical prote
1412	62.5	3.7	1412	2	T32650	hypothetical prote
1413	62.5	3.7	1413	2	B96695	hypothetical prote
1414	62	3.7	1414	2	T07861	germination-specif
1415	62	3.7	1415	2	AF3156	hypothetical prote
1416	62	3.7	1416	2	C98131	hypothetical prote

1417	62	3.7	156	2	T44233	hypothetical prote
1418	62	3.7	161	2	F72861	AcOrf-93 protein -
1419	62	3.7	200	2	D87521	Cog7 family protei
1420	62	3.7	227	2	H95231	conserved hypothet
1421	62	3.7	232	2	D71432	hypothetical prote
1422	62	3.7	258	2	T38373	hypothetical prote
1423	62	3.7	264	2	A81668	conserved hypothet
1424	62	3.7	282	2	A35084	fibrinogen-related
1425	62	3.7	290	2	H81832	hypothetical prote
1426	62	3.7	294	2	T21474	hypothetical prote
1427	62	3.7	309	2	B82460	hypothetical prote
1428	62	3.7	326	1	VGXR7H	glycoprotein VP7 p
1429	62	3.7	326	1	VGXRMD	glycoprotein VP7 p
1430	62	3.7	326	1	VGXRWA	glycoprotein VP7 p
1431	62	3.7	334	2	T29672	hypothetical prote
1432	62	3.7	339	2	B34895	transcription fact
1433	62	3.7	341	2	S54079	snRNP-associated p
1434	62	3.7	342	1	F64141	probable L-iditol
1435	62	3.7	344	2	T28729	hypothetical prote
1436	62	3.7	349	2	G81697	fructose-bisphosph
1437	62	3.7	350	2	G01950	hypothetical prote
1438	62	3.7	352	2	H43763	nonstructural prot
1439	62	3.7	353	2	C70502	hypothetical prote
1440	62	3.7	354	1	S17953	alkanal monooxygen
1441	62	3.7	358	2	S23111	connexin 40 - mous
1442	62	3.7	358	2	T23802	hypothetical prote
1443	62	3.7	359	2	H85823	hypothetical prote
1444	62	3.7	359	2	B90977	hypothetical prote
1445	62	3.7	363	2	T39527	hypothetical prote
1446	62	3.7	374	2	AG3337	transcription regu
1447	62	3.7	385	2	T18821	hypothetical prote
1448	62	3.7	387	2	D75417	acyl-CoA dehydroge
1449	62	3.7	387	2	A86302	hypothetical prote
1450	62	3.7	389	2	B65182	bacteriophage N4 a
1451	62	3.7	394	2	T21759	hypothetical prote
1452	62	3.7	398	2	AF0529	1-deoxy-D-xyulose
1453	62	3.7	402	2	G83289	conserved hypothet
1454	62	3.7	406	2	C81017	amino-acid N-acety
1455	62	3.7	407	2	T37865	probable MYST-fami
1456	62	3.7	410	2	C64831	ycaQ protein - Esc
1457	62	3.7	416	1	KFBO	coagulation factor
1458	62	3.7	420	2	H86331	F6F9.9 protein - A
1459	62	3.7	421	2	B64819	yblu protein - Esc
1460	62	3.7	424	2	T26997	hypothetical prote
1461	62	3.7	433	2	T27538	hypothetical prote
1462	62	3.7	449	2	T44643	galactosyl transfe
1463	62	3.7	463	2	T41390	zinc finger protei
1464	62	3.7	464	2	T20238	hypothetical prote
1465	62	3.7	476	2	G84634	probable prollycar
1466	62	3.7	483	2	AD1223	hypothetical prote
1467	62	3.7	497	2	E81987	hypothetical prote
1468	62	3.7	509	2	F81041	cytoplasmic axial
1469	62	3.7	515	2	T00510	probable cytochrom
1470	62	3.7	517	2	T43358	hnf-3/forkhead tra
1471	62	3.7	521	2	AB0269	anthranilate synth
1472	62	3.7	527	2	AE2932	Na+/H+ antiporter
1473	62	3.7	543	2	T16015	hypothetical prote
1474	62	3.7	549	2	T16016	hypothetical prote
1475	62	3.7	550	2	B98350	hypothetical prote
1476	62	3.7	570	2	AC2356	hypothetical prote
1477	62	3.7	575	2	AD0453	lisocitrate dehydr
1478	62	3.7	575	2	B64174	hypothetical prote
1479	62	3.7	580	2	C81352	lipid export ABC t
1480	62	3.7	593	1	DTCHPH	purh bifunctional
1481	62	3.7	600	2	T04267	NPRI protein homol
1482	62	3.7	604	2	S57065	probable membrane
1483	62	3.7	605	2	D82434	probable conserved
1484	62	3.7	684	2	T33785	hypothetical prote
1485	62	3.7	689	2	S60306	BPF-1 protein - pa
1486	62	3.7	699	1	S38982	kinesin-related pr
1487	62	3.7	721	2	T05815	hypothetical prote
1488	62	3.7	731	2	T09172	probable calcium-a
1489	62	3.7	736	2	S59136	estradiol 17beta-d

1490	62	3.7	762	2	C69657	cobalamin-independ
1491	62	3.7	789	2	T45762	vacuolar sorting p
1492	62	3.7	799	2	T00052	hypothetical prote
1493	62	3.7	819	1	TVCHFG	fibroblast growth
1494	62	3.7	819	2	A96567	hypothetical prote
1495	62	3.7	837	2	B82932	preprotein translo
1496	62	3.7	838	2	JC7363	95K retinoblastoma
1497	62	3.7	844	2	S61104	BR01 protein - yea
1498	62	3.7	859	2	F84981	leucine-cRNA ligas
1499	62	3.7	906	2	E84948	NADH2 dehydrogenas
1500	62	3.7	937	2	I53282	gene PACB4 protein

ALIGNMENTS

RESULT 1
JC7110
brain-specific membrane anchor protein - human
C/Species: Homo sapiens (man)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: JC7110
R/Elson, G.C.A.; de Coignac, A.B.; Aubry, J.P.; Delneste, Y.; Magistrelli, G.; Holzwarth
Biochem. Biophys. Res. Commun. 264, 55-62, 1999
A/Title: BSMAP, a novel protein expressed specifically in the brain whose gene is local1
A/Reference number: JC7110; MUID:99458621; PMID:10527841
A/Accession: JC7110
A/Molecule type: mRNA
A/Residues: 1-342 <EL>
A/Cross-references: UNIPROT:Q9UK28; GB:AF186264; NID:g6003653; PIDN:AAF00529.1; PID:g600
C/Genetics:
A/Map position: 19p12
C/Superfamily: human brain-specific membrane anchor protein
C/Keywords: brain; glycoprotein; membrane bound; transmembrane protein

Query Match 25.0%; Score 423.5; DB 2; Length 342;
Best Local Similarity 33.5%; Pred. No. 3.7e-29;
Matches 107; Conservative 56; Mismatches 115; Indels 41; Gaps 8;

QY	16	LPPLLLTMTALA---GSGGTASAEAFDSVLTGDTFASCHRAQLTYPLHTYPEKEEL-----	67
Db	7	MBPPLLLLLLLASPPASAPSARDPFAQLGDTQNCQLRCR-DRDLGPQPSQGLEGASE	65
QY	68	-----YACQRCGLFSICQFVDDGIDLNRTKLCEESACTEAYSQSDSEQYACHLGCQ	118
Db	66	SPYDRAVLISACERGCRLFSICRFVARSSKPNATQTECEAAVEAYVKEAQACSHGCW	125
QY	119	NQLPFAELROQLSIMPKNHLLPPLTVRSFMSDMDSAQSFTSSWTFYIQADDGKIV	178
Db	126	SQPAPEPEQKRVLEAPSGALSL-LDLFSTLCNDLVNSAQGFVSSWTWYVLQTDNGKV	184
QY	179	IFQSKPEIQ---YAPHLEQEPNLRRES-----SLSKM--SYLQMNSSQAH	219
Db	185	VFQTOPIVESLGFQGRLLQRVETWRGSHPEALEVHVDPVGPLDKVRKAKIRYKSSKAK	244
QY	220	NFLDEGSDGFLRCLSLNSG---WILTTVLVSVMVLLMICCATVATAVEQYVSEKLSI	276
Db	245	VESEEPQDNDFLSCMRRSGLPRWILACCLFLSVLVMWLWSCSTLVTA PGHLKFPQLTL	304
QY	277	YGDLEFPMNEQKLNRYPASS	295
Db	305	EQHKGFMEPDWPLYPPPS	323

RESULT 2
T29551
hypothetical protein C16D9.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T29551
R/Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, July 1996

A/Description: The sequence of *C. elegans* cosmid C16D9.
A/Reference number: Z20640
A/Accession: T29551
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-2380 <GAT>
A/Cross-references: EMBL:U64858, PIDN:AAB18281.1, GSPDB:GN00023, CESP:C16D9.2
A/Experimental source: strain Bristol N2; clone C16D9
C/Genetics:
A/Gene: CESP:C16D9.2
A/Map position: 5
A/Introns: 45/3; 70/3; 116/1; 252/3; 316/1; 365/1; 473/2; 508/1; 531/1; 596/2; 681/3; 721

Query Matchn	6.0%;	Score 102;	DB 2;	Length 2380;
Best Local Similarity	21.7%;	Pred. No. 3.6;		
Matches 65;	Conservative 38;	Mismatches 97;	Indels 100;	Gaps 16

QY	34	SAEAFDVLGDTASCHRAQ---	LTYPILHT-----	YPKEEELLYACRGCRLLFSIC	80
Db	25	SATVRESSL---KTCQSQCEERNL	AYPLDSCGEVHTGLAEYNYSSRIS	SCRGCE-----	76
QY	81	QFVDDGIDLNRTKLECSACTEAY	SQSDSEQYACHLGCQNQL-PFAELRQEQ	ILMSLMPKH	139
		:::	:::	:::	
Db	77	-----DVDERESKCDVKCSEEGIVSN---	ACKQGCRAVLVSFLAQQAQALLI	QVHVNME	126
QY	140	LL-----FPLTLVRS-----	FMSDMMDSAQSFITSSWTFY	LQADGKIVIFQ	181
		:::	:::	:::	
Db	127	VLETSMKLKMEFPETILABELKEIANADI	FWFSQTKPLNGILGWRWT-----		172
QY	182	SKPEIQYAPHLEQEPNTNLRESSLSKM---	SYLQMRNSQAHRNPLEDGESD	GFLRC	233
			:::	:::	
Db	173	SLPQ-----NSFRNSSLSESVHVPFEHGEHVE	VRLLALSYRNQVLVSRTTYHLP		221
QY	234	LSLNSGWILTTLLVLSVMVL---	LWICCATVATAVEQYVPSEKLSI	YGDLFEMNEQKLN	289
			:::	:::	
Db	222	LS-KSG-----TTLEVIGQLQSLDDRAVAVCYRT---	NQPTPKFKLTIM---	TLNDNTIN	268

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RESULT 3
T46488
hypothetical protein DKFP434J065.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T46488
R/Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, January 2000
A/Reference number: Z23035
A/Accession: T46488
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-741 <AAA>
A/Cross-references: UNIPROT:Q8NDE6; EMBL:AL137638
A/Experimental source: adult testis; clone DKFP434J065
C/Genetics:
A/Note: DKFP434J065.1

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	Query Match	Best Local Similarity	Score	DB 2;	Length	Gaps
	Matches	65; Conservative	95.5; Pred. No. 3.3; Mismatches	118; Indels	131; Gaps	15;
QY	31	GTASAEAFDSVLGDTASCHRACOLTYPLHTYPEKEELYACQ-----RGCRLFSI	79			
Dd	305	GKTCAKLSDSCALGD-----HGCE-----HSCVSSSEDSFVCQCFEGYILREDGKTCRRKD	354			
QY	80	CQFVDDGIDLNRTKLECESACTEAYSQSDEQYAC-----HL	115			
Dd	355	CQAIDHG-----CEHCIV-----NSDDSYTCECLEGFRLAEDGKRCKRKDVCKSTHH	401			
QY	116	GCQN-----QLPFAELRQEQMLSLMPKMHLLEPLLVRSFWSMDMDSAQS	160			
Dd	402	GCEHLCVNNNGNSYICCKSGEGFVLADGGRRCKCKCTEGPIDLVFIIDGSKSLGBENFEVVQ	461			

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QY      161 FITTSWTFYLQADDGKIVIFOSKE-----IYAPHLEOEPTNLRESSISKMSYLQMKN 214  
        ||::|||::||::|||::||:  
Db      462 FVT-----GIIDSLTISPRAVGLLOYSTOVHTEFT-LRNFSAK----DMKK 505  
  
QY      215 SOAHNRFLEDGESDG-----FLRCISLNSGWILTTTLVLVSWMLLWICATVATAVEOY 268  
        :||::|||::||  
Db      506 AVAHHKYMKGSGMTGLALKHMFERSFTOGEG-----ARPLSTR 543  
  
QY      269 VPSEKLSTGYD-----LEFMNEOKLNRRYPASSLVVRSKTEDHEEAGPLPTKVNI,AHS 321  
        ||::|||::|||::|||::||:  
Db      544 VPRAL-VFTDGRADVDSEWASKAKANGITMYAVGVKAIEELQETIASEPNTNGHLFYA 602  
  
QY      322 E 322  
        |  
Db      603 E 603
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RESULT 4
A57513
heat shock protein 110k - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57513; S51311
R;Lee-Yoon, D.; Easton, D.; Murawski, M.; Burd, R.; Subjeck, J.R.
J. Biol. Chem. 270, 15725-15733, 1995
A;Title: Identification of a major subfamily of large hsp70-like proteins through the cl
A;Reference number: A57513; MUID:95318163; PMID:7797574
A;Accession: A57513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-858 <LEE>
A;Cross-references: UNIPROT:Q60446; GB:Z47807; NID:g633180; PIDN:CAA87768.1; PID:g633181
R;Yoon, D.; Murawski, M.J.; Burd, R.; Easton, D.P.; Subjeck, J.R.
submitted to the EMBL data library, January 1995
A;Description: Identification of a major subfamily of large hsp70-like proteins through
A;Reference number: S51311
A;Accession: S51311
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-858 <YOO>
A;Cross-references: EMBL:Z47807; NID:g633180; PIDN:CAA87768.1; PID:g633181
C;Superfamily: heat shock protein 91
C;Keywords: heat shock; stress-induced protein

Query Match      5.5%; Score 92.5; DB 2; Length 858;
Best Local Similarity 21.3%; Pred. No. 7.2;
Matches 62; Conservative 47; Mismatches 89; Indels 93; Gaps 14;

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[illegible]

RESULT 5
G71557
probable glucanotransferase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis

Db 1297 ALQGTSAQIKAKLKEIAEKVELELKVSSSTS-----ELT-----KKESEVFQLOE- 1344

QY 74 CRLFSICQFVDDGIDLNRTKLECESACT-----EAYSQSDQYACHLGCONLPFAELRQ 128

Db 1345 -----QINKQGLEIESLKTIVSHAEVAHESLQOKL-----ESSQQLAGL-- 1384

QY 129 EQLMSLMPKMHLLFPLTLVR-----SFWSDMMDSAQSFTSSWTFYLLQADDGKIVIFQSKP 184

Db 1385 EHLRELQPKDELQKLSKKEEDVSYSGQLSEKEALTKIQTBIEQED-LIKALHTQL 1443

QY 185 EIQYAPH-----LEQEPNLRSSLSKMSYLOMRNSQA-----HRNPLEDGES 227

Db 1444 EMQAKEHDERIKQLOVELCEMKQKPEIGEESRAKOI--QRKLQALISRKEALKENKS 1501

QY 228 DGFRLCLSLNSGWI--LTTTLVLSVMVLWICCATVATAVEQYVPS--EKLSTYGDLEF 282

Db 1502 --LOEELSLARGTIERLTKSL-----ADVESQVSAQNKEKDTVLGRLLAL 1543

QY 283 MNE-----QKLNRYPASSLVVVRSKTEDHEE 308

Db 1544 LQERDKLITEMDRSLLENQSLSSCESLKLALGELTEDEK 1585

RESULT 12

T00361
hypothetical protein KIAA0678 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00361
R/Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A/Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A/Reference number: 214142; MUID:98403880; PMID:9734811
A/Accession: T00361
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1021 <ISH>
A/Cross-references: UNIPROT:O75165; EMBL:AB014578; NID:g3327169; PIDN:BAA31653.1; PID:g3
C/Experimental source: brain; clone HK02710
A/Genetics:
A/Note: KIAA0678

Query Match 5.0%; Score 84.5; DB 2; Length 1021;

Best Local Similarity 18.8%; Pred. No. 44;

Matches 68; Conservative 51; Mismatches 133; Indels 109; Gaps 16;

QY 20 LLTLMALAGSGSTASAEAFDSV-----LGDTSACHRACQLTTPHLYPKE-----E 65

Db 554 LIFSLLRVHAGQYQQLALEVNVITSNQDCVNNIAESMWLSSLLALHLSLSSRQLVLE 613

QY 66 ELYACQRCRLFSICQFVDDGIDLNRTKLECESACTEAYSQSDEQYACHLGCONLPFAE 125

Db 614 TLYALTSTKTIK-----EAMAKGALITYLLDMFCNSTHPQVR 650

QY 126 LROEQLMSLMPKMHLLFP--LTLVRSFWSMDMDSAQSFTSSWTFYLLQADDGKIVIFQ- 181

Db 651 AQTAELEFAKMTADKLIQPKVRITLMKFLPSVFMDAMR-----DNDEAAVHIFEG 699

QY 182 --SKPEIQYAPH-LEQEPNLRSSLSKMSYLOMRNSQAHRNPLED-----GESDG---- 229

Db 700 THENPELIMWNSRDKVSTTVREMLEHFKN-QQDNPEANWKLPEDEAVVFGAEAGELAV 758

QY 230 ---FLRCLSLNSGWL-----TTTLV-----LSVMVLWICCATVATA 264

Db 759 GGVFLRIFIAQPAVNLKRPREFLIALLEKLTLEKNNPHGETLETTLMATVCLFSAQPO 818

QY 265 VEQYVPSEKSTYGDL---EFMNEQKLNRYPASSLVVVRSKTEDH-----EEAGP 311

Db 819 LADQVPP-----LGHLPKVIQAMNHRN-NAIPKSAIRVITHALSENELCVRAMASLETTGP 872

QY 312 L 312

Db 873 L 873

RESULT 13

T30845

probable DNA repair protein RAD50 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C/Accession: T30845

R/Kim, K.K.; Daud, A.I.; Wong, S.C.; Pajak, L.; Tsai, S.C.; Wang, H.; Henzel, W.J.; Fiel

J. Biol. Chem. 271, 29255-29264, 1996

A/Title: Mouse RAD50 has limited epitopic homology to p53 and is expressed in the adult

A/Reference number: 220899; MUID:97067183; PMID:8910585

A/Accession: T30845

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1312 <KIM>

A/Cross-references: UNIPROT:P70388; EMBL:U66887; NID:g1575574; PID:g1575575; PIDN:AACS28

C/Genetics:

A/Map position: 11

C/Superfamily: RAD50 protein

C/Keywords: DNA repair

Query Match 5.0%; Score 84; DB 2; Length 1312;

Best Local Similarity 21.7%; Pred. No. 65;

Matches 65; Conservative 46; Mismatches 106; Indels 82; Gaps 15;

QY 63 KEEELYACQRCRLFSICQFVDDGIDLNRTKLECE-----SACTEAYSQ-----SD 108

Db 618 KEEQLSSYED--KLFDVCGSQDLBSDLGRLEKEIEKSSKORAMLAGATVAVYSQFITQLTD 675

QY 109 EQYACHLGCONLPFAELRQEQQLMSLMPKMHLLFPLTLVRSFWSMDMDSAQSFTSSWTF 168

Db 676 ENQSCCPVCQVRVQTEABLQEVISDLSQKRLA-----PDKLSTSESLKKK--- 722

QY 169 YLQADD--GKIVIFQSKPEIQYAPHLEQEPNLRSSLSKMSYLOMRNSQAHRNPLEDGE 226

Db 723 ERRRDEMLGLVYVRSQSIIDLK-----EKEIPELR-NRLQSVN---RDIQRLKNDIBEQE 772

QY 227 SDGFLRCLSLNSGWI--LTTTLVLSVMVLWICCATVATAVEQY-----VPSEKLSI 276

Db 773 T-----LGTIMPEESAKV---CLTDVTIMERFQMLKQVERKIAQQAAL 816

QY 277 YG-----DLFENNEQKLNRYPASSLVVVRSKTE-----DHEAGPLPTKVNLAHSE 322

Db 817 QGVDLDRTVQGVNQEQEK--QHRLDPTVTSKTELNRKLIQDQEQEQIQLHLSKTNELKSE 873

RESULT 14

T13254

nitric-oxide synthase (EC 1.14.13.39) - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T13254

R/Regulski, M.; Tuilly, T.

Proc. Natl. Acad. Sci. U.S.A. 92, 9072-9076, 1995

A/Title: Molecular and biochemical characterization of dNOS: A Drosophila Ca/calmodulin-

A/Reference number: 217642; MUID:96016111; PMID:7568075

A/Accession: T13254

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1350 <REG>

A/Cross-references: UNIPROT:Q27571; EMBL:U25117; NID:g1000081; PID:g1000082; PIDN:AAC468

C/Genetics:

A/Gene: NOS

A/Cross-references: FlyBase:FBgn0011676

A/Map position: 2

C/Function:

A/Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH ;

C/Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihinomoprotein reduct

C/Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal

F;329/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 5.0%; Score 84; DB 2; Length 1350;
Best Local Similarity 22.6%; Pred. No. 68;
Matches 76; Conservative 42; Mismatches 133; Indels 86; Gaps 18;

Search completed: March 28, 2005, 13:11:03
Job time : 40 secs

QY 14 LGLPILLLLTMALAG-GSGTASAEAFDSVLGDTASCHRAQQLTYPLHTYPEKEELIYACQR 72
Db 1031 LTPPSRQLLTLLAGFCEDTADKERLELLVNDSSAYEDWRHRLP-HLLDVLEEFPSCRP 1089
QY 73 GC-----RLFSIC---QFVDDGIDLN--RTKLECESACTEAYSQSDQYACHL 115
Db 1090 PAPLLLAQLTPLQPRFYRYSISSPRRVSDEIHLTVAIVKRCED-----GQGDERYGV-- 1141
QY 116 GCQNQLPFAELRQEQMLSLMPKMLLF-----PLTLV-----RSFMS----- 152
Db 1142 -CSNYL--SGLRADDELFMFVRSAIGFHLPSDRSRPITLIGPGTGIAFPRSFQGFQVLR 1198
QY 153 DMMDSAQSFITSSWTFYLAQDDGKIVIFQSKPEIQYAPHLEQEPNTL-RESSLSKMSYLQ 211
Db 1199 DLDPTAK--LPKMWLFPGCRNRDVLVYAEKAEQLQDQILDVFLALSREQALPK-TYVQ 1255
QY 212 MRNSQAHRNPLEDESDGFLRCLSLNSGWILTTTLVLSVMVLLMICATVATAVEQYVPS 271
Db 1256 -----DLIEQEFDSL.YQLIVQERGHIVV-----CGDVTMAEHVYQTI 1292
QY 272 EKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEE 308
Db 1293 RK-CIAG-----KEQKSEAEVETFTLLTRDESRYHED 1323

RESULT 15
S31805
VP5 protein - porcine rotavirus
C/Species: porcine rotavirus
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S31805
R;Xu, L.; Tian, Y.; Tarlow, O.; McCrae, M.A.
submitted to the EMBL Data Library, May 1992
A/Reference number: S31783
A/Accession: S31805
A/Status: preliminary
A/Molecule type: genomic RNA
A/Residues: 1-486 <XUL>
A/Cross-references: UNIPROT:Q85037; EMBL:Z12107; NID:g61354; PIDN:CAAV78092.1; PID:g61355
A/Experimental source: strain OSY
C;Superfamily: bovine rotavirus nonstructural protein NCVP2

Query Match 4.9%; Score 83.5; DB 2; Length 486;
Best Local Similarity 20.8%; Pred. No. 22;
Matches 65; Conservative 37; Mismatches 114; Indels 97; Gaps 15;

QY 48 CHRAQQLTYPLHTYPEKEELIYACQRGLFSICQ-----FVDDG----- 86
Db 42 CLDCCQ-----HT-----DLTYC-RGCTMYHVCQWCQYGRGFLDNEPHLLRMRTFKNEV 90
QY 87 -----IDLNRTKLECESACTEAYSQSDQYACHLGCQNQLPFAELRQEQMLSLMPKM 138
Db 91 TKDGLMNLVDMFDTLFPMNQKIYDFINNTROHKCRNECVNQW-----YN 135
QY 139 HLLPPLTL-----VRSFWSMDMDSAQ---SFTSSWTF-YLQADDGKIYIFQ 181
Db 136 HLLMPITLQSLSLIEDGDVYVIFGYDDMNNVNQTFPSFVNLVDIYDKLLDDVNFT--- 192
QY 182 SKPEIQYAPHLEQEPNTLRESSLSKMSYLQMR---NSQAHRNPLEDESDGF-----LRC 233
Db 193 ---RMSFLPVTLLQOEYALRYFSKSRFISEQRKCVSDSRFSINVLENLHNPSPKMQITRNC 249
QY 234 LSLNSGWILTTTLVLSVMVLLMICATVATAVEQYVPSEKLSIYGDLFEMNEQKLNRYPA 293
Db 250 NELSSDMNGACKLVKDT SAYFNI---LKTSHVEFYSISTRGVF-----TQRKLK--IA 298
QY 294 SSLVVVRSKTEDH 306
Db 299 SKLIKPNYITSNH 311

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 28, 2005, 13:08:45 ; Search time 58 Seconds
(without alignments)
2851.751 Million cell updates/sec

Title: US-09-978-299A-330

Perfect score: 1694

Sequence: 1 MAAPKGSILWRTQLGLPPL.....EDHEAGPLPTKVNLAHSEI 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: uniprot_03:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1694	100.0	323	1 CA08_HUMAN	Q9bxs4 homo sapien
2	1674.5	98.8	324	2 Q96KX7	Q96kx7 homo sapien
3	1611	95.1	323	1 CA08_MOUSE	Q9gy73 mus musculu
4	1234	72.8	239	2 Q6P5R1	Q6p5r1 homo sapien
5	993.5	58.6	324	2 Q6GNB1	Q6gnb1 xenopus lae
6	957.5	56.5	318	2 Q8QFS3	Q8qfs3 tetraodon n
7	905	53.4	309	2 Q8UWE8	Q8uwe8 tetraodon n
8	595.5	35.2	339	2 Q7T2E2	Q7t2e2 brachydanio
9	423.5	25.0	342	1 BMAP_HUMAN	Q9uk28 homo sapien
10	415.5	24.5	337	2 Q7TN12	Q7tn12 mus musculu
11	104	6.1	832	2 Q8IYZ6	Q8iyz6 homo sapien
12	102	6.0	1250	2 Q8I7I3	Q8i7i3 caenorhabdi
13	102	6.0	2456	2 Q8I7I3	Q8i7i3 caenorhabdi
14	100	5.9	808	2 Q6ZQC8	Q6zqc8 mus musculu
15	96.5	5.7	768	2 Q972I5	Q972i5 leishmania
16	96.5	5.7	858	2 Q66HA8	Q66ha8 rattus norv
17	96	5.7	937	2 Q96FT5	Q96ft5 homo sapien
18	95.5	5.6	537	2 Q96AA0	Q96aa0 homo sapien
19	95.5	5.6	715	2 Q7Z5X1	Q7z5x1 homo sapien
20	95.5	5.6	915	2 Q6UWA5	Q6uwa5 homo sapien
21	95.5	5.6	1016	2 Q8NDE6	Q8nde6 homo sapien
22	94	5.5	517	2 Q8H883	Q8h883 oryza sativ
23	94	5.5	1312	2 Q9JIL8	Q9jil8 rattus norv
24	93.5	5.5	956	1 MTN2_HUMAN	Q00339 homo sapien
25	92.5	5.5	858	1 H105_CRIGR	Q60446 cricetus
26	91	5.4	407	2 Q6C994	Q6c994 yarrowia li
27	90	5.3	616	2 Q9W1F4	Q9w1f4 drosophila
28	89	5.3	971	2 Q7YS79	Q7ys79 canis fami
29	89	5.3	1124	1 PHVA_LATSA	P93673 lachyrus sa
30	88.5	5.2	527	1 MALQ_CHLTR	O84089 chlamydia t
31	88.5	5.2	527	2 Q6YW20	Q6yw20 oryza sativ

32	88.5	5.2	703	2 Q7S872	Q7s872 neurospora
33	88.5	5.2	817	2 Q9S2T4	Q9szt4 arabidopsis
34	88	5.2	1349	2 Q7YU33	Q7yuh3 drosophila
35	87.5	5.2	142	2 Q9H1H9	Q9hin9 thermoplasma
36	87.5	5.2	523	2 Q7T5A5	Q7t5a5 onion yello
37	87.5	5.2	662	2 Q9F7S3	Q9f7s3 gamma-prote
38	87.5	5.2	937	1 YM92_CAEEL	P34531 caenorhabdi
39	87	5.1	693	2 Q9DG20	Q9dgt0 gallus gall
40	87	5.1	736	2 Q9FVC7	Q9fvc7 oryza sativ
41	86.5	5.1	327	2 Q66CU1	Q66cu1 yersinia ps
42	86.5	5.1	327	2 Q8ZGL2	Q8zgl2 yersinia pe
43	86.5	5.1	535	2 Q8MT44	Q8mt44 drosophila
44	86.5	5.1	535	2 Q9VDZ3	Q9vdz3 drosophila
45	86.5	5.1	1030	2 Q6LL68	Q6ll68 photobacter
46	86	5.1	389	1 SUCC_XANCP	Q8p676 xanthomonas
47	86	5.1	429	2 Q74CB2	Q74cb2 geobacter s
48	86	5.1	641	2 Q7Y0Y5	Q7y0y5 gossypium h
49	86	5.1	850	2 Q6AJK1	Q6ajk1 desulfotale
50	86	5.1	894	2 Q8XSY3	Q8xey3 ralstonia s
51	85.5	5.0	330	2 Q87SV6	Q87sv6 vibrio para
52	85.5	5.0	398	1 DXR_PHOLL	Q7n8p3 photorhabdu
53	85.5	5.0	558	2 Q6NXX0	Q6nux0 brachydanio
54	85.5	5.0	579	2 Q8NFG4	Q8nfg4 homo sapien
55	85.5	5.0	717	2 Q6LZ17	Q6lzl7 methanococc
56	85.5	5.0	1212	2 Q7Q9W7	Q7q9w7 anopheles g
57	85.5	5.0	1389	2 Q6DRM6	Q6drme brachydanio
58	85.5	5.0	3259	1 GOB1_HUMAN	Q14789 homo sapien
59	85	5.0	337	2 Q6MPI1	Q6mpi1 bdellovibri
60	85	5.0	356	1 GBA3_NEUCR	Q9hfw7 neurospora
61	85	5.0	467	2 Q9EXY5	Q9exy5 escherichia
62	85	5.0	678	1 LGP2_MOUSE	Q99j87 mus musculu
63	84.5	5.0	450	2 Q6C655	Q6c655 yarrowia li
64	84.5	5.0	486	2 Q84940	Q84940 porcine rot
65	84.5	5.0	858	2 Q75EX3	Q75ex3 ashbya goss
66	84.5	5.0	1021	1 DJCD_HUMAN	Q75165 homo sapien
67	84.5	5.0	1375	2 Q6ZUT5	Q6zut5 homo sapien
68	84	5.0	395	2 Q7PJZ4	Q7pjz4 anopheles g
69	84	5.0	445	2 Q8XZFS	Q8xzfs ralstonia s
70	84	5.0	476	2 Q94F80	Q94f80 zea mays (m
71	84	5.0	570	2 Q6A0A5	Q6a0a5 mus musculu
72	84	5.0	858	1 H105_MOUSE	Q61699 mus musculu
73	84	5.0	858	2 Q8C430	Q8c430 mus musculu
74	84	5.0	858	2 Q8VCW6	Q8vcw6 mus musculu
75	84	5.0	869	2 Q65ZC5	Q65zcs caenorhabdi
76	84	5.0	1312	2 P70388	P70388 mus musculu
77	84	5.0	1349	1 NOS_DROME	Q27571 drosophila
78	84	5.0	5729	2 Q8I622	Q8i622 plasmodium
79	83.5	4.9	376	2 Q96ML4	Q96ml4 homo sapien
80	83.5	4.9	486	1 VN53_ROTTHW	P35424 human rotav
81	83.5	4.9	486	2 Q85037	Q85037 porcine rot
82	83.5	4.9	623	2 Q6ZU80	Q6zu80 homo sapien
83	83.5	4.9	678	2 Q64ZJ4	Q64zj4 bacteroides
84	83.5	4.9	700	2 Q6BX81	Q6bx81 debaryomyce
85	83.5	4.9	1020	2 Q43254	O43254 homo sapien
86	83.5	4.9	1318	2 Q6CNX5	Q6cnx5 kluveromyc
87	83.5	4.9	1397	2 Q6PQD5	Q6pqd5 sus scrofa
88	83.5	4.9	3056	2 Q6BG85	Q6bg85 paramecium
89	83.5	4.9	3622	2 Q6DF00	Q6df00 xenopus tro
90	83	4.9	278	2 Q9VZV5	Q9vzv5 drosophila
91	83	4.9	412	2 Q6I603	Q6i603 oryza sativ
92	83	4.9	421	2 Q6DCN1	Q6dcn1 xenopus lae
93	83	4.9	433	2 Q95LTS	Q95lts macaca fasc
94	83	4.9	461	2 Q9JSH1	Q9jsh1 chlamydia p
95	83	4.9	500	2 Q9Z8T3	Q9z8t3 chlamydia p
96	83	4.9	503	2 Q9K258	Q9k258 chlamydia p
97	83	4.9	735	1 LMGI_MOUSE	Q7qk26 anopheles g
98	83	4.9	1607	2 Q8V708	P02468 mus musculu
99	82.5	4.9	326	2 Q8CAC0	O8v708 bovine rota
100	82.5	4.9	566	2 Q8QZS3	Q8cac0 mus musculu
101	82.5	4.9	579	2 Q7R677	Q8qz83 mus musculu
102	82.5	4.9	1703	2 Q9UAX8	Q7r677 giardia lam
103	82.5	4.9	308	2	Q9uax8 caenorhabdi
104	82	4.8			

105	82	4.8	389	1	SUCC_XANAC	Q8ph15 xanthomonas
106	82	4.8	469	2	Q6CT13	Q6ct13 kluyveromyc
107	82	4.8	621	2	Q6LMP4	Q6lmp4 methanococc
108	82	4.8	626	1	BGAL_LEULA	Q02603 leuconostoc
109	82	4.8	1299	2	Q847C8	Q847c8 nodularia s
110	82	4.8	1349	2	Q964G1	Q964g1 pseudocentr
111	82	4.8	1564	2	Q6PGP7	Q6pgp7 homo sapien
112	82	4.8	1568	2	Q15077	Q15077 homo sapien
113	82	4.8	2804	1	NEBL_HUMAN	Q6kc79 homo sapien
114	82	4.8	2804	2	Q6IEH8	Q6ieh8 homo sapien
115	81.5	4.8	247	2	Q6HKX3	Q6hcx3 bacillus th
116	81.5	4.8	264	1	RCIT_BPP4	P13059 bacterioph
117	81.5	4.8	381	2	Q8DK45	Q8dk45 synecchococc
118	81.5	4.8	438	2	Q6MTB4	Q6mtb4 mycoplasma
119	81.5	4.8	525	1	VCL_THECC	Q43358 theobroma c
120	81.5	4.8	775	2	Q7SD99	Q7sd99 neurospora
121	81.5	4.8	778	2	Q9SJU6	Q9sjj6 arabidopsis
122	81.5	4.8	937	2	Q7XRN6	Q7xrn6 oryza sativ
123	81.5	4.8	996	1	VGNM_RCMV	P13561 red clover
124	81.5	4.8	1020	2	Q6FK73	Q6fk73 candida gla
125	81.5	4.8	1063	2	Q7Q548	Q7q548 anopheles g
126	81.5	4.8	1173	2	Q9UP86	Q9up86 homo sapien
127	81.5	4.8	1312	2	Q92878	Q92878 homo sapien
128	81	4.8	477	2	P94005	P94005 lycopersico
129	81	4.8	485	1	1A12_LYCES	P18485 lycopersico
130	81	4.8	485	2	Q6EHI3	Q6ehi3 lycopersico
131	81	4.8	485	2	Q66773	Q66773 equine rota
132	81	4.8	504	2	Q64R82	Q64r82 bacteroides
133	81	4.8	635	2	Q6AHQ4	Q6ahq4 caenorhabdi
134	81	4.8	723	2	Q6GMT7	Q6gmt7 homo sapien
135	81	4.8	774	2	Q8S3P4	Q8s3p4 oryza sativ
136	81	4.8	848	2	Q9PE39	Q9pe39 xylella fas
137	81	4.8	1032	2	Q97PS6	Q97ps6 streptococc
138	81	4.8	1032	2	Q8DP39	Q8dp39 streptococc
139	81	4.8	1609	1	LMG1_HUMAN	P11047 homo sapien
140	81	4.8	2798	1	NPBL_MOUSE	Q6kcd5 mus musculu
141	80.5	4.8	282	1	NADA_APLKU	Q27312 aplysia kur
142	80.5	4.8	426	2	Q8BWX1	Q8bwx1 mus musculu
143	80.5	4.8	453	2	Q64767	Q64767 avian adeno
144	80.5	4.8	459	1	FA9_MOUSE	P16294 mus musculu
145	80.5	4.8	471	2	Q6VEL7	Q6vp17 salmonella
146	80.5	4.8	471	2	Q9EXV9	Q9exv9 salmonella
147	80.5	4.8	475	1	ATXX_MOUSE	P28658 mus musculu
148	80.5	4.8	563	2	Q7RX55	Q7rx55 neurospora
149	80.5	4.8	608	2	Q6MT71	Q6mt71 mycoplasma
150	80.5	4.8	661	2	Q23611	Q23611 arabidopsis
151	80.5	4.8	720	2	Q19718	Q19718 caenorhabdi
152	80.5	4.8	904	2	Q8A1K1	Q8a1k1 bacteroides
153	80.5	4.8	956	2	Q99K64	Q99k64 mus musculu
154	80.5	4.8	1430	2	Q9VMA7	Q9vma7 drosophila
155	80.5	4.8	2042	2	Q6TXG6	Q6txg6 rattus norv
156	80.5	4.8	2342	2	Q65980	Q65980 cherry viru
157	80.5	4.8	2386	1	EFL4_HUMAN	Q7z7m0 homo sapien
158	80	4.7	119	1	MOT1_PIG	P01307 sus scrofa
159	80	4.7	188	2	Q95JH3	Q95jh3 trichosurus
160	80	4.7	266	2	Q8PAV4	Q8pav4 xanthomonas
161	80	4.7	455	2	Q6C960	Q6c960 yarrowia li
162	80	4.7	486	2	Q41178	Q41178 porcine rot
163	80	4.7	486	2	P87724	P87724 rotavirus a
164	80	4.7	491	1	VN53_ROTBR	P12475 bovine rota
165	80	4.7	575	2	Q9VVP2	Q9vvp2 drosophila
166	80	4.7	614	2	Q9K5S1	Q9k5s1 bacillus ha
167	80	4.7	1224	2	Q6PC15	Q6pc15 xenopus lae
168	80	4.7	1580	2	Q754A4	Q754a4 ashbya goss
169	80	4.7	2042	2	Q7Q3U4	Q7q3u4 anopheles g
170	80	4.7	4207	2	Q7R3Y5	Q7r3y5 giardia lam
171	79.5	4.7	335	2	Q7QD23	Q7qd23 anopheles g
172	79.5	4.7	395	2	Q9DC34	Q9dc34 mus musculu
173	79.5	4.7	406	2	Q68EQ9	Q68eq9 xenopus tro
174	79.5	4.7	435	2	Q765H8	Q765h8 flaveria tr
175	79.5	4.7	469	1	TBG2_ORYSA	Q49068 oryza sativ
176	79.5	4.7	486	2	Q82013	Q82013 human rotav
177	79.5	4.7	579	2	Q76JQ2	Q76jq2 rattus norv
178	79.5	4.7	600	2	Q17401	Q17401 caenorhabdi
179	79.5	4.7	632	2	Q6GN05	Q6gn05 xenopus lae
180	79.5	4.7	682	2	Q6ZMN9	Q6zmn9 homo sapien
181	79.5	4.7	702	2	Q8TEJ1	Q8tej1 homo sapien
182	79.5	4.7	793	2	Q7RDY3	Q7rdy3 plasmodium
183	79.5	4.7	837	2	Q6P4A6	Q6p4a6 homo sapien
184	79.5	4.7	838	1	POSN_MOUSE	Q62009 mus musculu
185	79.5	4.7	848	2	Q754R5	Q754r5 ashbya goss
186	79.5	4.7	971	2	Q6CT54	Q6ct54 kluyveromyc
187	79.5	4.7	971	2	Q6ZW11	Q6zwi1 homo sapien
188	79.5	4.7	999	2	Q9NQ36	Q9nq36 homo sapien
189	79.5	4.7	1136	2	P87224	P87224 neurospora
190	79.5	4.7	1866	2	Q86WI3	Q86wi3 homo sapien
191	79.5	4.7	1984	2	Q9QBH1	Q9qbh1 viral hemor
192	79.5	4.7	1984	2	Q9QJW0	Q9qjw0 viral hemor
193	79.5	4.7	1984	2	Q9WME7	Q9wme7 viral hemor
194	79.5	4.7	2330	1	EFL4_MOUSE	P60882 mus musculu
195	79	4.7	193	2	Q6UBI9	Q6ubi9 nostoc sp.
196	79	4.7	301	2	Q8C2T7	Q8c2t7 mus musculu
197	79	4.7	305	2	Q9DG21	Q9dg21 gallus gall
198	79	4.7	399	1	HMP_BACSU	P49852 bacillus su
199	79	4.7	431	2	Q97GG9	Q97g93 clostridium
200	79	4.7	445	2	Q9XGG3	Q9xgg3 phalaenopsi
201	79	4.7	449	2	Q754Y6	Q754y6 ashbya goss
202	79	4.7	459	2	Q86ME2	Q86me2 caenorhabdi
203	79	4.7	536	2	Q9J2L9	Q9j2l9 rhesus monk
204	79	4.7	545	1	SECY_SPIOL	P93690 spinacia ol
205	79	4.7	618	2	Q7QT58	Q7qt58 giardia lam
206	79	4.7	661	2	Q6PEB0	Q6peb0 mus musculu
207	79	4.7	714	2	Q68005	Q68005 enterococcu
208	79	4.7	790	2	Q6CLM7	Q6clm7 yarrowia li
209	79	4.7	846	2	Q84FU0	Q84fu0 chlamydia t
210	79	4.7	846	2	Q84FU1	Q84fu1 chlamydia t
211	79	4.7	846	2	Q84FU3	Q84fu3 chlamydia t
212	79	4.7	846	2	Q84FU5	Q84fu5 chlamydia t
213	79	4.7	891	2	Q8GHT8	Q8ght8 pseudomonas
214	79	4.7	1072	2	Q80YS4	Q80ys4 mus musculu
215	79	4.7	1122	1	TIE2_MOUSE	Q02858 mus musculu
216	79	4.7	1124	1	PHYA_PEA	P15001 pisum sativ
217	79	4.7	1357	1	MYP_STRPU	P19615 stronglyloce
218	79	4.7	1578	2	Q9AV25	Q9av25 oryza sativ
219	79	4.7	1726	2	Q8UVK2	Q8uvk2 brachydanio
220	79	4.7	1726	2	Q6PAU2	Q6pau2 brachydanio
221	79	4.7	193	2	Q6FIU8	Q6fiu8 candida gla
222	78.5	4.6	341	2	Q9KC57	Q9kc57 bacillus ha
223	78.5	4.6	377	2	Q6D035	Q6d035 erwinia car
224	78.5	4.6	377	2	O08806	O08806 mus musculu
225	78.5	4.6	377	2	Q80Y29	Q80y29 mus musculu
226	78.5	4.6	453	2	Q6SJ47	Q6sj47 escherichia
227	78.5	4.6	453	2	Q9WTG1	Q9wtg1 plasmid r10
228	78.5	4.6	460	2	Q6P4J7	Q6p4j7 xenopus tro
229	78.5	4.6	479	2	Q6DC80	Q6dc80 brachydanio
230	78.5	4.6	521	1	FAEB_ASPNG	Q8wzi8 aspergillus
231	78.5	4.6	553	2	Q8ZJY4	Q8zjy4 salmonella
232	78.5	4.6	668	2	Q9XX27	Q9xx27 caenorhabdi
233	78.5	4.6	705	2	Q66IN0	Q66in0 xenopus lae
234	78.5	4.6	785	2	Q6U818	Q6u818 myxococcus
235	78.5	4.6	843	2	Q86JDI	Q86jdi dictyosteli
236	78.5	4.6	1087	2	Q86BS5	Q86bs5 drosophila
237	78.5	4.6	1124	2	Q8MOJ8	Q8mqj8 drosophila
238	78.5	4.6	1127	2	P89531	P89531 dengue viru
239	78.5	4.6	1436	2	Q9LFY6	Q9lfy6 arabidopsis
240	78.5	4.6	1449	2	Q8YWC0	Q8ywc0 anabaena sp
241	78.5	4.6	1984	2	Q9QBH5	Q9qbh5 viral hemor
242	78.5	4.6	2619	2	Q6YKX3	Q6yk39 bacillus su
243	78	4.6	277	2	Q8FI02	Q8fi02 escherichia
244	78	4.6	327	2	Q9NDY9	Q9ndy9 leishmania
245	78	4.6	348	2	Q7Q5H5	Q7q5h5 anopheles g
246	78	4.6	366	2	Q8FGQ4	Q8fgq4 escherichia
247	78	4.6	370	2	Q9LHO3	Q9lhq3 arabidopsis
248	78	4.6	458	2	Q81PE8	Q81pe8 bacillus an
249	78	4.6	468	2	Q63A90	Q63a90 bacillus ce
250	78	4.6	538	2	Q6BC96	Q6bc96 mumps virus

251	78	4.6	564	1	YUES_CAEEL	P90859 caenorhabdi	324	77	4.5	481	2	Q831B5	Q831b5 enterococcu
252	78	4.6	601	2	Q8E1J1	Q8e1j1 shewanella	325	77	4.5	491	2	Q8JZ13	Q8jz13 bovine rota
253	78	4.6	624	2	Q94487	Q94487 schizosacch	326	77	4.5	597	2	Q8L4C7	Q8l4c7 arabidopsis
254	78	4.6	645	2	Q91Q73	Q91q73 influenza c	327	77	4.5	599	2	Q7N219	Q7n219 photorhabdu
255	78	4.6	655	2	Q617C1	Q617c1 influenza c	328	77	4.5	640	2	Q84MH1	Q84mh1 oryza sativ
256	78	4.6	700	2	Q8WS94	Q8ws94 caenorhabdi	329	77	4.5	645	2	Q91Q74	Q91q74 influenza c
257	78	4.6	828	2	Q6FL29	Q6fl29 candida gla	330	77	4.5	647	2	Q8MLX3	Q8mlx3 caenorhabdi
258	78	4.6	846	2	Q83TT8	Q83tc8 chlamydia t	331	77	4.5	647	2	Q8MM25	Q8mm25 caenorhabdi
259	78	4.6	846	2	Q84FU2	Q84fu2 chlamydia t	332	77	4.5	647	2	Q8MV49	Q8mv49 caenorhabdi
260	78	4.6	846	2	Q84FU4	Q84fu4 chlamydia t	333	77	4.5	647	2	Q8MV50	Q8mv50 caenorhabdi
261	78	4.6	927	2	Q823X9	Q823x9 chlamydophi	334	77	4.5	647	2	Q8MV51	Q8mv51 caenorhabdi
262	78	4.6	1114	2	Q8S6D2	Q8s6d2 oryza sativ	335	77	4.5	647	2	Q8MV52	Q8mv52 caenorhabdi
263	78	4.6	1189	2	Q8RKW7	Q8rkw7 providencia	336	77	4.5	647	2	Q8MV53	Q8mv53 caenorhabdi
264	78	4.6	3898	2	Q68535	Q68535 classical s	337	77	4.5	647	2	Q8MV54	Q8mv54 caenorhabdi
265	77.5	4.6	166	2	Q8YPM1	Q8ypw1 anabaena sp	338	77	4.5	661	2	Q9TVY6	Q9tvye caenorhabdi
266	77.5	4.6	287	2	Q9UT16	Q9ut16 schizosacch	339	77	4.5	714	2	Q60149	Q60149 streptococc
267	77.5	4.6	324	1	FEZ2_RAT	P97578 rattus norv	340	77	4.5	719	1	PRH1_SCHPO	Q03319 schizosacch
268	77.5	4.6	348	2	Q76LH9	Q76lh9 rattus norv	341	77	4.5	846	2	Q83U50	Q83u50 chlamydia t
269	77.5	4.6	375	2	Q76LH1	Q76lh1 rattus norv	342	77	4.5	846	2	Q84FT9	Q84ft9 chlamydia t
270	77.5	4.6	414	2	Q9UM44	Q9um44 homo sapien	343	77	4.5	858	1	H105_HUMAN	Q92598 homo sapien
271	77.5	4.6	417	2	Q6PFG7	Q6pfg7 mus musculu	344	77	4.5	878	1	PMPI_CHLTR	Q6k8d6 oryza sativ
272	77.5	4.6	425	1	PLA2_MOUSE	Q9ers5 mus musculu	345	77	4.5	1037	2	Q6K8D6	Q9qw24 rattus sp.
273	77.5	4.6	462	1	GAAS_HUMAN	P31644 homo sapien	346	77	4.5	1083	2	Q9QW24	Q9up95 homo sapien
274	77.5	4.6	463	1	SCB1_MOUSE	Q9z219 mus musculu	347	77	4.5	1085	1	S124_HUMAN	Q9y2h3 homo sapien
275	77.5	4.6	463	2	Q8BHJ7	Q8bhj7 m mus muscu	348	77	4.5	1578	2	Q9Y2H3	Q7Yy83 cryptospori
276	77.5	4.6	464	1	GAAS_RAT	P19969 rattus norv	349	77	4.5	2255	1	FRS1_MOUSE	Q8ot14 mus musculu
277	77.5	4.6	464	2	Q9D4Z5	Q9d4z5 mus musculu	350	77	4.5	4010	1	Q6LFZ0	Q6lfz0 photobacter
278	77.5	4.6	503	1	NQRB_CHLCV	Q823p2 chlamydophi	351	76.5	4.5	193	2	Q9CLD2	Q9cld2 pasteurella
279	77.5	4.6	530	1	VC04_SWPVK	P32228 swinepox vi	352	76.5	4.5	254	2	Q9CLD2	Q9cld2 pasteurella
280	77.5	4.6	530	2	Q8V3S6	Q8v3s6 swinepox vi	353	76.5	4.5	352	2	Q86FF1	Q86ff1 schistosoma
281	77.5	4.6	545	1	TM26_PIG	Q77666 sus scrofa	354	76.5	4.5	363	2	Q8DRC8	Q8drc8 streptococc
282	77.5	4.6	597	1	NUCD_BUCBP	Q89au4 buchnera ap	355	76.5	4.5	375	2	Q94K53	Q94k53 arabidopsis
283	77.5	4.6	632	2	Q69T22	Q69t22 oryza sativ	356	76.5	4.5	449	2	O04496	O04496 arabidopsis
284	77.5	4.6	639	2	Q9FLA9	Q9fla9 arabidopsis	357	76.5	4.5	458	2	Q6HNM2	Q6hnm2 bacillus th
285	77.5	4.6	641	2	Q8MQM0	Q8mqm0 drosophila	358	76.5	4.5	465	2	Q8KE83	Q8ke83 chlorobium
286	77.5	4.6	646	2	Q23521	Q23521 caenorhabdi	359	76.5	4.5	471	2	Q90577	Q90577 gallus gall
287	77.5	4.6	657	1	CSP1_CORGL	Q01377 corynebacte	360	76.5	4.5	501	2	Q6NUV7	Q6nuv7 brachydanio
288	77.5	4.6	665	2	Q38925	Q38925 arabidopsis	361	76.5	4.5	531	2	Q6DJ55	Q6dj55 xenopus tro
289	77.5	4.6	665	2	Q9FFE29	Q9ff29 arabidopsis	362	76.5	4.5	556	2	Q8H023	Q8h023 oryza sativ
290	77.5	4.6	669	2	Q9SZD5	Q9szd5 arabidopsis	363	76.5	4.5	564	2	Q883V6	Q883v6 pseudomonas
291	77.5	4.6	696	2	Q9S793	Q9s793 arabidopsis	364	76.5	4.5	569	2	Q98435	Q98q45 mycoplasma
292	77.5	4.6	701	2	Q8CN81	Q8cn81 staphylococ	365	76.5	4.5	570	2	Q96M46	Q96m46 homo sapien
293	77.5	4.6	753	2	Q90Z75	Q90z75 dromaius no	366	76.5	4.5	597	2	Q7X914	Q7x914 oryza sativ
294	77.5	4.6	753	2	Q90Z76	Q90z76 dromaius no	367	76.5	4.5	607	2	Q7FA04	Q7fa04 oryza sativ
295	77.5	4.6	760	2	Q920P3	Q920p3 m bmp/retin	368	76.5	4.5	657	2	Q6FJ72	Q6fj72 candida gla
296	77.5	4.6	760	2	Q925T8	Q925t8 rattus norv	369	76.5	4.5	657	2	Q83ZP3	Q83zp3 corynebacte
297	77.5	4.6	760	2	Q8C1C9	Q8c1c9 mus musculu	370	76.5	4.5	717	2	Q95JW2	Q95jw2 macaca fasc
298	77.5	4.6	761	2	Q9QXL0	Q9qx10 mus musculu	371	76.5	4.5	745	2	Q67PP5	Q67pps symbiobacte
299	77.5	4.6	761	2	Q7ZZR3	Q7zzr3 gallus gall	372	76.5	4.5	809	2	Q7Q5H7	Q7q5h7 anopheles g
300	77.5	4.6	800	2	Q9KPY4	Q9kfy4 bacillus ha	373	76.5	4.5	810	2	Q8C435	Q8c435 mus musculu
301	77.5	4.6	810	2	Q6GUA3	Q6gua3 mus musculu	374	76.5	4.5	956	1	MTN2_MOUSE	O08746 mus musculu
302	77.5	4.6	853	2	Q9Y1Y4	Q9y1y4 ephydattia f	375	76.5	4.5	956	2	Q8R542	Q8r542 mus musculu
303	77.5	4.6	890	1	GLND_SALTI	Q8z9a7 salmonella	376	76.5	4.5	979	2	Q7XSX6	Q7sx66 brachydanio
304	77.5	4.6	890	1	GLND_SALTY	P23679 salmonella	377	76.5	4.5	1191	2	Q9VUY8	Q9vuy8 drosophila
305	77.5	4.6	892	2	Q25243	Q25243 lucilia cup	378	76.5	4.5	1331	2	Q9VUY8	Q90w93 poecilia re
306	77.5	4.6	959	2	Q6PUA9	Q6puu9 ambystoma m	379	76.5	4.5	1666	2	Q8MXG2	Q8mxg2 caenorhabdi
307	77.5	4.6	1078	2	Q9VSS9	Q9vss9 drosophila	380	76.5	4.5	1949	2	Q8MXG3	Q8mxg3 caenorhabdi
308	77.5	4.6	1099	2	Q69K21	Q69k21 oryza sativ	381	76.5	4.5	1960	2	Q812E3	Q812e3 mus musculu
309	77.5	4.6	1259	1	CAML_RAT	Q05695 rattus norv	382	76.5	4.5	2009	2	Q9VXM0	Q9vxm0 drosophila
310	77.5	4.6	1654	2	C7SEM6	Q7sem6 ashbya goss	383	76.5	4.5	2895	1	HYD_DROME	P51592 drosophila
311	77.5	4.6	1984	2	Q9QJV4	Q9qjv4 viral hemor	384	76	4.5	152	2	Q8ZMR9	Q8zmr9 salmonella
312	77.5	4.6	2653	2	Q25253	Q25253 lucilia cup	385	76	4.5	160	2	Q8C239	Q8c239 mus musculu
313	77.5	4.6	3124	2	Q6FJ13	Q6fj13 candida gla	386	76	4.5	160	2	Q8C254	Q8c254 mus musculu
314	77.5	4.5	286	2	Q8AXC0	Q8axc0 xenopus lae	387	76	4.5	243	1	TLP1_CASSA	Q9smh2 castanea sa
315	77	4.5	288	2	Q9DG22	Q9dgd2 gallus gall	388	76	4.5	247	2	Q81FJ8	Q81fj8 bacillus ce
316	77	4.5	330	2	Q9KP40	Q9kp40 vibrio chol	389	76	4.5	265	2	Q8S5X7	Q8s5x7 oryza sativ
317	77	4.5	364	2	Q9T099	Q9t099 arabidopsis	390	76	4.5	277	1	HEMK_ECOLI	Q8nv67 escherichia
318	77	4.5	374	2	Q6CQ14	Q6cq14 kluyveromyc	391	76	4.5	293	2	Q8NV67	Q8nv67 staphylococ
319	77	4.5	375	2	Q7OT29	Q7ot29 bixa orella	392	76	4.5	375	2	Q8Y572	Q8y572 listeria mo
320	77	4.5	392	2	Q6VTN6	Q6vtn6 choristoneu	393	76	4.5	381	2	Q6BLY2	Q6bly2 debaryomyce
321	77	4.5	398	2	Q6CSZ3	Q6csz3 kluyveromyc	394	76	4.5	390	1	Y109_NPVOP	O10348 oryza pseu
322	77	4.5	472	2	Q8T8U6	Q8t8u6 drosophila	395	76	4.5	450	2	Q9VH28	Q9vh28 drosophila
323	77	4.5	475	1	ARCD_LACSK	O53092 lactobacill	396	76	4.5	464	1	YMG8_YEAST	Q04638 saccharomyc

397	76	4.5	485	2	Q9PWC0	Q9pwc0	gallus gall
398	76	4.5	486	2	Q82043	Q82043	human rotav
399	76	4.5	486	2	Q82045	Q82045	human rotav
400	76	4.5	491	2	Q86194	Q86194	human rotav
401	76	4.5	551	2	Q9DIC6	Q9dic6	lettuce nec
402	76	4.5	572	2	Q19594	Q19594	caenorhabdi
403	76	4.5	598	2	Q6D799	Q6d799	erwinia car
404	76	4.5	609	2	Q82674	Q82674	influenza c
405	76	4.5	648	1	HEMA_INCYB	P87691	influenza c
406	76	4.5	652	2	Q8IMX7	Q8imx7	drosophila
407	76	4.5	663	2	Q6BJR4	Q6bjr4	debaryomyce
408	76	4.5	673	2	Q8IMX6	Q8imx6	drosophila
409	76	4.5	700	2	Q62299	Q62299	caenorhabdi
410	76	4.5	745	2	Q8EH07	Q8eh07	shewanella
411	76	4.5	830	2	Q17995	Q17995	caenorhabdi
412	76	4.5	869	2	Q8TLI4	Q8tli4	methanosarc
413	76	4.5	942	2	Q9JU01	Q9jj01	mus musculu
414	76	4.5	1299	2	Q9YUJ1	Q9ytj1	ateline her
415	76	4.5	1471	1	MY51_SCHPO	Q74805	schizosacch
416	76	4.5	1509	2	Q75AF6	Q75af6	ashbya goss
417	76	4.5	1687	2	Q61204	Q61204	mus musculu
418	76	4.5	1828	1	MY5A_RAT	Q9qyf3	rattus norv
419	76	4.5	1855	1	MY5A_HUMAN	Q9y4l1	homo sapien
420	76	4.5	1911	2	Q8H7V4	Q8h7v4	oryza sativ
421	76	4.5	1980	2	Q991N2	Q991n2	little cher
422	76	4.5	2025	2	Q99PP2	Q99pp2	mus musculu
423	76	4.5	2581	2	Q8ZS63	Q8zs63	anabaena sp
424	76	4.5	4699	2	Q9V383	Q9v383	drosophila
425	75.5	4.5	213	2	Q9PP57	Q9pp57	campylobact
426	75.5	4.5	233	2	Q7MJG7	Q7mjg7	vibrio vuln
427	75.5	4.5	237	2	Q83909	Q83909	ovine adeno
428	75.5	4.5	247	2	Q81SN8	Q81sn8	bacillus an
429	75.5	4.5	264	2	Q8BMW1	Q8bmw1	m mus muscu
430	75.5	4.5	282	2	Q7SX78	Q7sx78	brachydanio
431	75.5	4.5	304	1	PLA2_HUMAN	Q9hb19	homo sapien
432	75.5	4.5	330	2	Q8P9W4	Q8p9w4	xanthomonas
433	75.5	4.5	363	2	Q97ST2	Q97st2	streptococc
434	75.5	4.5	406	2	Q6INE8	Q6ine8	xenopus lae
435	75.5	4.5	410	2	Q80919	Q80919	arabidopsis
436	75.5	4.5	414	2	Q9ZVW6	Q9zvw6	arabidopsis
437	75.5	4.5	430	2	Q8BHX9	Q8bhx9	mus musculu
438	75.5	4.5	447	2	Q8ZPB1	Q8zpb1	salmonella
439	75.5	4.5	453	2	Q82905	Q82905	escherichia
440	75.5	4.5	464	2	Q7QYA9	Q7qya9	giardia lam
441	75.5	4.5	474	2	Q9FRU9	Q9fru9	nicotiana t
442	75.5	4.5	474	2	Q9LEC3	Q9lec3	nicotiana t
443	75.5	4.5	476	2	Q6RYT1	Q6ryt1	pfaffia mos
444	75.5	4.5	497	2	Q6GQA9	Q6gqa9	xenopus lae
445	75.5	4.5	513	2	Q7TPS8	Q7tps8	mus musculu
446	75.5	4.5	535	2	Q9FZL3	Q9fzl3	nicotiana t
447	75.5	4.5	546	2	Q8BTR8	Q8btr8	mus musculu
448	75.5	4.5	547	2	P97531	P97531	rattus norv
449	75.5	4.5	547	2	Q99LI0	Q99li0	mus musculu
450	75.5	4.5	547	2	Q6P744	Q6p744	rattus norv
451	75.5	4.5	562	2	Q7V9F1	Q7v9f1	prochloroco
452	75.5	4.5	591	2	Q8W433	Q8w433	gentiana lu
453	75.5	4.5	603	2	Q8R433	Q8r433	mus musculu
454	75.5	4.5	603	2	Q8CJ53	Q8cj53	mus musculu
455	75.5	4.5	628	2	Q6AMC4	Q6amc4	desulfotale
456	75.5	4.5	698	2	Q709D7	Q709d7	fusarium ox
457	75.5	4.5	749	2	Q9LHT9	Q9lht9	oryza sativ
458	75.5	4.5	754	1	UBP9_YEAST	P39967	saccharomyc
459	75.5	4.5	907	2	Q6MIL5	Q6mil5	bdellovibri
460	75.5	4.5	988	2	Q9XIF2	Q9xif2	arabidopsis
461	75.5	4.5	1092	2	Q6ZJ20	Q6zj20	oryza sativ
462	75.5	4.5	1201	2	Q8DAL0	Q8dal0	vibrio vuln
463	75.5	4.5	1284	2	Q74842	Q74842	schizosacch
464	75.5	4.5	1515	2	Q6AVS6	Q6av56	oryza sativ
465	75.5	4.5	1630	2	Q8PTF5	Q8ptf5	methanosarc
466	75.5	4.5	1659	2	Q7ROL2	Q7rq12	plasmodium
467	75.5	4.5	1837	2	Q9LU53	Q9lu53	arabidopsis
468	75.5	4.5	2472	2	Q8IIP3	Q8ilp3	plasmodius
469	75	4.4	213	2	Q93HW9	Q93hw9	magnetospir

Q8axc1	xenopus lae
Q8f7c7	leptospiira
Q8xdf2	escherichia
Q99ru5	staphylococ
Q7a3z5	staphylococ
Q6gea6	staphylococ
Q6rj01	corynebacte
Q9vyc0	drosophila
Q8yuj4	anabaena sp
Q9dgd3	gallus gall
Q6fgi9	acinetobact
Q7qnt4	anopheles g
P56680	humicola in
Q12622	humicola gr
Q9cic9	lactococcus
Q8k1f8	mus musculu
Q9vac8	drosophila
Q938q5	lactobacill
P30212	human rotav
Q84150	chlamydia t
Q96m34	homo sapien
Q9wrt5	macaca mula
Q807p1	mumps virus
Q6nct9	xenopus lae
Q62991	rattus norv
Q8brf7	mus musculu
Q8b077	influenza c
Q8wvm8	homo sapien
Q91q69	influenza c
Q91q66	influenza c
Q8w2r3	oryza sativ
Q7xgr2	oryza sativ
O13971	schizosacch
Q9ca47	arabidopsis
Q9alu6	pseudomonas
P53273	saccharomyc
Q28677	oryctolagus
Q6c2g1	yarrowia li
Q91pk1	arabidopsis
P10894	bos taurus
Q9sef7	arabidopsis
Q9c7y1	arabidopsis
Q9fh39	arabidopsis
Q8zav4	yersinia pe
Q8dip6	yersinia pe
Q6rsh4	strongyloce
Q6nr96	xenopus lae
Q9c1g0	kallischroma
Q68872	classical s
Q9j7j9	rattus norv
Q65c86	bacillus li
Q7mdz4	vibrio vuln
Q8d734	vibrio vuln
Q8sr11	encephalito
O17591	caenorhabdi
Q6nuy9	brachydanio
Q92pu9	rhizobium m
Q26424	crassostrea
Q9qj45	human herpe
Q97kes	clostridium
Q758k5	ashbya goss
Q6emf4	escherichia
Q9m421	hordeum vul
Q75a43	ashbya goss
Q9er24	rattus norv
P21614	mus musculu
Q7v9r3	prochloroco
Q96zr6	leishmania
Q9wt43	human herpe
P27964	human papil
Q92828	homo sapien
O12899	homo sapien
Q7yr34	pan troglod

543	74.5	4.4	542	2	Q6IWL4	Q6iwl4 brachydanio
544	74.5	4.4	542	2	Q7SXX1	Q7sxx1 brachydanio
545	74.5	4.4	590	2	Q9BGY1	Q9bgy1 macaca fasc
546	74.5	4.4	596	2	Q8N7W0	Q8n7w0 homo sapien
547	74.5	4.4	603	2	Q7WAN3	Q7wan3 bordetella
548	74.5	4.4	605	2	Q7WJT6	Q7wjt6 bordetella
549	74.5	4.4	620	2	Q7VWR3	Q7vwr3 bordetella "
550	74.5	4.4	673	2	Q9ZMY7	Q9zmy7 helicobacte
551	74.5	4.4	691	2	Q6ESV5	Q6esv5 oryza sativ
552	74.5	4.4	696	2	Q9BWX9	Q9bwx9 homo sapien
553	74.5	4.4	699	2	Q73QH0	Q73qh0 treponema d
554	74.5	4.4	716	2	Q93875	Q93875 caenorhabdi
555	74.5	4.4	717	2	Q8NA44	Q8na44 homo sapien
556	74.5	4.4	719	2	Q8NCS7	Q8ncs7 homo sapien
557	74.5	4.4	739	1	GCP4_MEDTR	Q9sc88 medicago tr
558	74.5	4.4	761	2	Q60477	Q60477 homo sapien
559	74.5	4.4	761	2	Q6PIA0	Q6pia0 homo sapien
560	74.5	4.4	833	2	Q8TBZ0	Q8tbz0 homo sapien
561	74.5	4.4	906	2	Q9M2B1	Q9m2b1 arabidopsis
562	74.5	4.4	1007	2	Q9M285	Q9m285 arabidopsis
563	74.5	4.4	1009	1	M2B2_HUMAN	Q9y2e5 homo sapien
564	74.5	4.4	1009	2	Q66MF2	Q66mp2 homo sapien
565	74.5	4.4	1009	2	Q86T67	Q86t67 homo sapien
566	74.5	4.4	1019	2	Q6BVH3	Q6bvh3 debaryomyce
567	74.5	4.4	1125	2	Q9ILI6	Q9ili6 turkey astr
568	74.5	4.4	1139	1	HMW1_MYCGB	Q49413 mycoplasma
569	74.5	4.4	1160	2	Q7SBL3	Q7sbl3 neurospora
570	74.5	4.4	1342	1	ERB3_HUMAN	P21860 homo sapien
571	74.5	4.4	1513	2	Q9VWK5	Q9vwx5 drosophila
572	74.5	4.4	1600	2	Q9SM84	Q9sm84 oryza sativ
573	74.5	4.4	3006	2	Q9Y4D8	Q9y4d8 homo sapien
574	74.5	4.4	3210	1	CENF_HUMAN	P49454 homo sapien
575	74.5	4.4	3343	2	Q8ORI9	Q8ori9 papaya ring
576	74	4.4	143	2	Q6ERH0	Q6erh0 oryza sativ
577	74	4.4	160	2	Q62NA4	Q62na4 bacillus li
578	74	4.4	243	2	Q8Y796	Q8y796 listeria mo
579	74	4.4	247	2	Q6AXU5	Q6axu5 rattus norv
580	74	4.4	320	2	Q8K6Z6	Q8k6z6 streptococc
581	74	4.4	326	2	Q42086	Q42086 human rotav
582	74	4.4	326	2	Q83441	Q83441 murine rota
583	74	4.4	346	2	Q9NDU0	Q9ndu0 drosophila
584	74	4.4	354	2	Q9SRV2	Q9srrv2 arabidopsis
585	74	4.4	410	2	Q8DV08	Q8dv08 streptococc
586	74	4.4	474	2	Q7P577	Q7p577 fusobacteri
587	74	4.4	476	2	Q8BJY5	Q8bjy5 mus musculu
588	74	4.4	489	2	Q8XZV1	Q8xzv1 ralsstonia s
589	74	4.4	504	2	Q64HC4	Q64hc4 pelteobagru
590	74	4.4	511	1	TXN2_BOVIN	Q9n2i8 bos taurus
591	74	4.4	520	2	Q7S6A5	Q7s6a5 neurospora
592	74	4.4	531	1	GPM1_MYCMS	Q6msf0 mycoplasma
593	74	4.4	559	2	Q6ST99	Q6st99 manheimia
594	74	4.4	579	2	Q8T4A3	Q8t4a3 drosophila
595	74	4.4	599	2	Q9LQ00	Q9lq00 arabidopsis
596	74	4.4	605	2	Q72QD0	Q72qd0 leptospira
597	74	4.4	605	2	Q8F5R7	Q8f5r7 leptospira
598	74	4.4	609	2	Q82673	Q82673 influenza c
599	74	4.4	626	2	Q88SE7	Q88se7 lactobacill
600	74	4.4	628	1	TSDI_ABIGR	Q24475 abies grand
601	74	4.4	641	2	Q8B079	Q8b079 influenza c
602	74	4.4	641	2	Q8B080	Q8b080 influenza c
603	74	4.4	641	2	Q8B081	Q8b081 influenza c
604	74	4.4	642	1	HEMA_INCTA	P07974 influenza c
605	74	4.4	646	2	Q674I7	Q674i7 influenza c
606	74	4.4	647	2	Q67386	Q67386 influenza c
607	74	4.4	648	1	HEMA_INCNB	Q67387 influenza c
608	74	4.4	649	2	Q674I8	Q674i8 influenza c
609	74	4.4	649	2	Q674I9	Q674i9 influenza c
610	74	4.4	649	2	Q9IQ70	Q9iq70 influenza c
611	74	4.4	649	2	Q9IQ71	Q9iq71 influenza c
612	74	4.4	650	2	Q9IQ67	Q9iq67 influenza c
613	74	4.4	682	2	Q6M930	Q6m930 neurospora
614	74	4.4	682	2	Q6DIDS	Q6did5 mus musculu
615	74	4.4	688	2	Q6VZY8	Q6vzy8 canarypox v
616	74	4.4	756	2	Q6FJY8	Q6fjy8 candida gla
617	74	4.4	776	2	Q6IR70	Q6ir70 xenopus lae
618	74	4.4	805	2	Q6LW47	Q6lw47 photobacter
619	74	4.4	818	2	Q9KB88	Q9kb88 bacillus ha
620	74	4.4	830	2	Q87E49	Q87e49 xylella fas
621	74	4.4	846	2	Q84FT7	Q84ft7 chlamydia t
622	74	4.4	846	2	Q84FT8	Q84ft8 chlamydia t
623	74	4.4	893	2	Q01596	Q01596 caenorhabdi
624	74	4.4	902	2	Q8S191	Q8s191 oryza sativ
625	74	4.4	907	2	Q04631	Q04631 arabidopsis
626	74	4.4	927	2	Q8BUL5	Q8bjl5 mus musculu
627	74	4.4	961	2	Q6ZQ92	Q6zq92 mus musculu
628	74	4.4	962	2	Q89443	Q89443 african swi
629	74	4.4	984	2	Q9GQN1	Q9gqn1 calliactis
630	74	4.4	984	2	Q9GQN2	Q9gqn2 calliactis
631	74	4.4	993	2	Q6S144	Q6s144 uncultured
632	74	4.4	1073	2	Q83C50	Q83c50 coxlella bu
633	74	4.4	1113	2	Q7Q4I6	Q7q4i6 anopheles g
634	74	4.4	1130	2	Q9XTI9	Q9xti9 caenorhabdi
635	74	4.4	1141	1	SRE2_HUMAN	Q12772 homo sapien
636	74	4.4	1193	2	Q86V36	Q86v36 homo sapien
637	74	4.4	1216	1	PIB1_MOUSE	Q9z1b3 mus musculu
638	74	4.4	1216	1	PIB1_RAT	P10687 rattus norv
639	74	4.4	1216	2	Q6PDH1	Q6pdh1 mus musculu
640	74	4.4	1487	1	LHN2_RAT	Q88923 rattus norv
641	74	4.4	1853	1	MYSA_MOUSE	Q99104 mus musculu
642	74	4.4	2073	1	BIME_EMENI	P24686 emericella
643	74	4.4	2156	1	RRPL_PUUMH	P27176 puumala vir
644	74	4.4	3924	1	ANK2_HUMAN	Q01484 homo sapien
645	73.5	4.3	143	2	Q9VA24	Q9va24 drosophila
646	73.5	4.3	217	2	Q7Q7W6	Q7q7w6 anopheles g
647	73.5	4.3	308	2	Q88TX0	Q88tx0 lactobacill
648	73.5	4.3	312	2	Q8LFP3	Q8lfp3 arabidopsis
649	73.5	4.3	328	2	Q8BGB3	Q8egb3 shewanella
650	73.5	4.3	330	2	Q18118	Q18118 caenorhabdi
651	73.5	4.3	340	2	Q63AT4	Q63at4 bacillus ce
652	73.5	4.3	360	2	Q7P5N9	Q7p5n9 fusobacteri
653	73.5	4.3	385	2	Q7VEL1	Q7vel1 prochloroco
654	73.5	4.3	386	1	ATP2_ARATH	Q01909 arabidopsis
655	73.5	4.3	414	2	Q6YUR1	Q6yur1 oryza sativ
656	73.5	4.3	417	2	Q8Y8X4	Q8y8x4 listeria mo
657	73.5	4.3	433	2	Q8DVJ0	Q8dvj0 streptococc
658	73.5	4.3	472	2	Q9DAP3	Q9dap3 mus musculu
659	73.5	4.3	505	2	Q9XIP2	Q9xip2 arabidopsis
660	73.5	4.3	537	2	Q9UIT6	Q9uit6 caenorhabdi
661	73.5	4.3	559	2	Q8CHX3	Q8chx3 mus musculu
662	73.5	4.3	609	2	Q8IJC3	Q8ijc3 plasmodium
663	73.5	4.3	673	2	Q24911	Q24911 helicobacte
664	73.5	4.3	680	2	Q8WPDI	Q8wpdi pimpla hypo
665	73.5	4.3	731	2	Q814B9	Q814b9 caenorhabdi
666	73.5	4.3	764	2	Q69X95	Q69x95 oryza sativ
667	73.5	4.3	796	2	Q9UIT5	Q9uit5 caenorhabdi
668	73.5	4.3	893	2	Q86PDS	Q86pds drosophila
669	73.5	4.3	893	2	Q9VRV8	Q9vrv8 drosophila
670	73.5	4.3	937	2	Q7RLB1	Q7rlb1 plasmodium
671	73.5	4.3	945	2	Q8N1W1	Q8n1w1 homo sapien
672	73.5	4.3	956	2	Q6FV21	Q6fv21 candida gla
673	73.5	4.3	958	2	Q8MWB5	Q8mwb5 trypanosoma
674	73.5	4.3	966	2	Q8CHD7	Q8chd7 mus musculu
675	73.5	4.3	998	2	Q8IXT1	Q8ixt1 homo sapien
676	73.5	4.3	1105	2	Q6FTE7	Q6fte7 candida gla
677	73.5	4.3	1106	2	Q6CXI7	Q6cxi7 kluveromyc
678	73.5	4.3	1184	2	Q7Q764	Q7q764 anopheles g
679	73.5	4.3	1229	2	Q7S9J9	Q7s9j9 neurospora
680	73.5	4.3	1235	1	KPB2_RABIT	P46018 oryctolagus
681	73.5	4.3	1317	2	Q7OZH3	Q7qzh3 giardia lam
682	73.5	4.3	1446	2	Q764I1	Q764i1 caenorhabdi
683	73.5	4.3	1561	2	Q8MRC6	Q8mrc6 drosophila
684	73.5	4.3	1561	2	Q9VX32	Q9vx32 drosophila
685	73.5	4.3	1564	2	Q95VZ5	Q95vz5 drosophila
686	73.5	4.3	1623	2	Q6A034	Q6a034 mus musculu
687	73.5	4.3	1667	2	Q6LON7	Q6lon7 picophilus
688	73.5	4.3	1739	2	Q7UK14	Q7uk14 rhodopirell

689	73.5	4.3	2204	2	Q913F4	Q913f4 newcastle d	762	72.5	4.3	326	2	Q7VUJ0	Q7vj10 helicobacte
690	73.5	4.3	2294	2	Q7QU56	Q7qu56 giardia lam	763	72.5	4.3	330	2	Q88CR3	Q88ct3 pseudomonas
691	73.5	4.3	2397	1	MOKB_SCHPO	Q09854 schizosacch	764	72.5	4.3	338	2	Q83E19	Q83e19 coxiella bu
692	73.5	4.3	2845	1	APC_MOUSE	Q61315 mus musculu	765	72.5	4.3	342	2	Q7MPC7	Q7mpc7 vibrio vuln
693	73.5	4.3	3153	2	Q6C6F9	Q6c6f9 yarrowia li	766	72.5	4.3	344	2	Q83Z52	Q83z52 uncultured
694	73	4.3	144	2	Q6RC41	Q6rc41 drosophila	767	72.5	4.3	344	2	Q8BMK7	Q8bmk7 mus musculu
695	73	4.3	238	2	O85093	O85093 pseudomonas	768	72.5	4.3	359	1	WECF_ECOLI	P56258 escherichia
696	73	4.3	276	1	NCT2_HUMAN	O95944 homo sapien	769	72.5	4.3	359	1	WECF_SHIFL	Q83ph8 shigella fl
697	73	4.3	295	2	Q6FJTL	Q6fjtl candida gla	770	72.5	4.3	366	2	Q6FT57	Q6ft57 candida gla
698	73	4.3	298	2	Q8U710	Q8u710 agrobacteri	771	72.5	4.3	371	2	Q7M8X9	Q7m8x9 wolinnella s
699	73	4.3	366	1	TORY_ECOLI	P52005 escherichia	772	72.5	4.3	377	2	Q92T54	Q92t54 rhizobium m
700	73	4.3	375	2	Q9UII4	Q9ui14 drosophila	773	72.5	4.3	390	2	Q66KX2	Q66kx2 xenopus lae
701	73	4.3	388	2	Q8R464	Q8r464 mus musculu	774	72.5	4.3	452	2	Q65OR4	Q65or4 bacteroides
702	73	4.3	390	2	Q7TLP9	Q7t1p9 choristoneu	775	72.5	4.3	456	2	Q6BJH0	Q6bjh0 debaryomyces
703	73	4.3	416	2	Q7MVL1	Q7mvl1 porphyromon	776	72.5	4.3	464	2	Q8KP24	Q8kp24 klebsiella
704	73	4.3	451	2	Q6ST57	Q6st57 human rhino	777	72.5	4.3	484	2	O48972	O48972 hordeum vul
705	73	4.3	458	2	Q736K9	Q736k9 bacillus ce	778	72.5	4.3	485	1	GLGA_BACST	Q08328 bacillus st
706	73	4.3	468	1	DNAB_MYCGE	P47340 mycoplasma	779	72.5	4.3	485	2	Q7VOR0	Q7v0r0 prochloroco
707	73	4.3	472	1	TBG_ANEPH	P34785 anemia phyl	780	72.5	4.3	504	2	Q8UI78	Q8ui78 agrobacteri
708	73	4.3	474	2	Q9W859	Q9w859 porcine ade	781	72.5	4.3	552	2	Q86SV6	Q86sv6 homo sapien
709	73	4.3	485	2	O57916	O57916 pyrococcus	782	72.5	4.3	574	1	Q636Z8	Q636z8 bacillus ce
710	73	4.3	485	2	O25870	O25870 helicobacte	783	72.5	4.3	582	2	Q8SV72	Q8sv72 encephalito
711	73	4.3	486	2	Q9IM71	Q9im71 human rotav	784	72.5	4.3	599	2	Q975V6	Q975v6 sulfolobus
712	73	4.3	491	2	Q76VV3	Q76vv3 rotavirus s	785	72.5	4.3	603	2	Q975V6	Q975v6 sulfolobus
713	73	4.3	491	2	Q89895	Q89895 bovine rota	786	72.5	4.3	619	2	Q9LL56	Q9ll56 oryza sativ
714	73	4.3	491	2	Q9WAA8	Q9waa8 human rotav	787	72.5	4.3	631	2	Q65QA7	Q65qa7 manheimia
715	73	4.3	494	2	O02641	O02641 caenorhabdi	788	72.5	4.3	640	2	Q90ZAI	Q90za1 xenopus lae
716	73	4.3	500	2	Q7XNLO	Q7xn10 oryza sativ	789	72.5	4.3	640	2	Q6BNU1	Q6bnu1 debaryomyce
717	73	4.3	544	2	Q6NB27	Q6nb27 rhodopsendo	790	72.5	4.3	645	1	VP74_NPVCF	P34053 choristoneu
718	73	4.3	546	2	Q9ADU0	Q9adu0 salmoneilla	791	72.5	4.3	660	2	Q7S125	Q7s125 neurospora
719	73	4.3	617	1	BFSI_RAT	Q02435 rattus norv	792	72.5	4.3	669	2	O04914	O04914 psilactum nu
720	73	4.3	635	2	Q9VUK7	Q9vuk7 drosophila	793	72.5	4.3	711	2	Q656W9	Q656w9 oryza sativ
721	73	4.3	644	1	NAH9_MOUSE	Q8bz00 mus musculu	794	72.5	4.3	721	2	Q66H87	Q66h87 rattus norv
722	73	4.3	663	2	Q6ME37	Q6me37 parachlamyd	795	72.5	4.3	736	2	Q7RRP2	Q7rrp2 plasmodium
723	73	4.3	668	1	ENV_FLVC6	P21443 feline leuk	796	72.5	4.3	750	1	GSH1_STRA3	Q8e3j9 streptococc
724	73	4.3	671	1	CHFA_BACSU	P29072 bacillus su	797	72.5	4.3	750	1	GSH1_STRAS	Q8d3m9 streptococc
725	73	4.3	688	2	Q9TYZ7	Q9tyz7 caenorhabdi	798	72.5	4.3	769	2	Q9PLI5	Q9pl15 chlamydia m
726	73	4.3	692	2	O9VI90	Q9vi90 drosophila	799	72.5	4.3	794	2	Q7XKV1	Q7xkv1 oryza sativ
727	73	4.3	715	2	Q84GX2	Q84gx2 photohabdu	800	72.5	4.3	836	1	YGL1_SCHPO	Q9y7j8 schizosacch
728	73	4.3	730	2	Q6L4A9	Q6l4a9 solanum dem	801	72.5	4.3	843	2	Q47802	Q47802 enterococcu
729	73	4.3	742	2	Q7QC58	Q7qc58 anopheles g	802	72.5	4.3	911	2	Q8GD70	Q8gdt0 helicobacill
730	73	4.3	813	2	Q7QI16	Q7qi16 anopheles g	803	72.5	4.3	931	2	Q7SE30	Q7se30 neurospora
731	73	4.3	814	2	Q9KPY1	Q9kpy1 vibrio chol	804	72.5	4.3	946	2	O07153	O07153 torpedo cal
732	73	4.3	844	2	Q6DD03	Q6dd03 xenopus lae	805	72.5	4.3	1036	2	O64819	O64819 arabidopsis
733	73	4.3	971	1	CSE1_PAGMA	Q9ptu3 pagrus majo	806	72.5	4.3	1075	2	MTR3_MOUSE	Q8k296 mus musculu
734	73	4.3	996	2	Q9FNF6	Q9fnp6 arabidopsis	807	72.5	4.3	1079	2	Q852G2	Q852g2 oryza sativ
735	73	4.3	1014	1	CIN1_YEAST	P40987 saccharomyc	808	72.5	4.3	1114	2	Q8GT16	Q8gt16 oryza sativ
736	73	4.3	1022	2	Q7Q9D9	Q7q9d9 anopheles g	809	72.5	4.3	1125	2	Q6K3D1	Q6k3d1 oryza sativ
737	73	4.3	1039	1	SYI_METUA	Q58357 methanococc	810	72.5	4.3	1159	2	Q66145	Q66145 mus musculu
738	73	4.3	1189	2	Q8KQU7	Q8kqu7 vibrio chol	811	72.5	4.3	1188	2	Q9USG8	Q9usg8 schizosacch
739	73	4.3	1216	1	PIB1_HUMAN	Q9nq66 homo sapien	812	72.5	4.3	1451	1	VGL2_CVCAI	Q9usg8 schizosacch
740	73	4.3	1221	2	Q9N5Z3	Q9n5z3 caenorhabdi	813	72.5	4.3	1466	2	O6YU44	P36300 canine ente
741	73	4.3	1259	2	Q6L4D7	Q6l4d7 oryza sativ	814	72.5	4.3	1508	1	GEM5_HUMAN	O6yu44 oryza sativ
742	73	4.3	1259	2	Q65XG9	Q65xg9 oryza sativ	815	72.5	4.3	1602	2	Q6BFF0	O8teg6 homo sapien
743	73	4.3	1336	2	Q6L3Q0	Q6l3q0 solanum dem	816	72.5	4.3	1858	2	Q7RXM6	Q6bff0 paramecium
744	73	4.3	1502	2	Q6C0U5	Q6c0u5 yarrowia li	817	72.5	4.3	2225	2	Q6RCQ4	Q6rcq4 legionella
745	73	4.3	1679	1	FUR2_DROME	Q7kz85 drosophila	818	72.5	4.3	2226	1	POLG_HPAV2	O6rcq4 legionella
746	73	4.3	1726	1	SUGH_HUMAN	Q62383 mus musculu	819	72.5	4.3	2264	2	Q6RKU2	P26580 h genome po
747	73	4.3	1726	1	SUGH_MOUSE	Q04592 mus musculu	820	72.5	4.3	2402	2	O9AER7	Q6rkj2 botrytis ci
748	73	4.3	1877	1	PCK5_MOUSE	Q8ie95 plasmodium	821	72.5	4.3	2667	2	Q7RWZ8	Q9aer7 staphylococ
749	73	4.3	2548	2	Q8IE95	Q8ie95 plasmodium	822	72.5	4.3	2735	2	Q8WZX6	Q7rwz8 neurospora
750	73	4.3	3025	2	Q962J9	Q962j9 mus musculu	823	72.5	4.3	2964	2	Q8I7W7	O8wxz6 neurospora
751	73	4.3	5327	1	MACF_MOUSE	Q9qxz0 mus musculu	824	72.5	4.3	3085	2	Q6XW15	O8l7w7 dictyosteli
752	73	4.3	177	1	CUF2_SCHPO	O94588 schizosacch	825	72.5	4.3	4969	2	Q8CF91	Q6xw15 beet mosali
753	72.5	4.3	180	2	Q7XI71	O7xi71 oryza sativ	826	72.5	4.3	5054	2	Q7RPJ1	Q8cf91 mus musculu
754	72.5	4.3	242	2	Q19919	Q19919 caenorhabdi	827	72.5	4.3	5165	2	Q8CF92	Q7rpj1 plasmodium
755	72.5	4.3	248	2	Q93MF0	Q93mf0 amycolatops	828	72.5	4.3	143	2	Q6RC97	Q8cf92 mus musculu
756	72.5	4.3	248	2	Q8C7C3	Q8c7c3 mus musculu	829	72	4.3	143	2	Q6RC97	Q6rc97 drosophila
757	72.5	4.3	255	2	Q83VG1	Q83vg1 lactococcus	830	72	4.3	143	2	Q6RC97	Q6rc97 drosophila
758	72.5	4.3	295	2	Q7YY99	Q7yy99 cryptospori	831	72	4.3	143	2	Q6RC97	Q6rc97 drosophila
759	72.5	4.3	303	2	Q92SA3	Q92sa3 rhizobium m	832	72	4.3	202	2	Q9GRC4	O6rc97 drosophila
760	72.5	4.3	311	2	Q6Q941	O6q941 uncultured	833	72	4.3	217	2	Q7TIC3	Q9grc4 megabalanus
761	72.5	4.3	322	2	Q82TH2	Q82th2 nitrosomona	834	72	4.3	222	2	Q91Z14	Q7lic3 ambystoma b

835	72	4.3	234	1	A29B_DROSI	Q9u968 drosophila	908	72	4.3	641	2	Q8B071	Q8b071 influenza c
836	72	4.3	245	2	Q7T0U7	Q7t0u7 xenopus lae	909	72	4.3	641	2	Q8B072	Q8b072 influenza c
837	72	4.3	251	2	Q7QWJ2	Q7qwj2 giardia lam	910	72	4.3	641	2	Q8B076	Q8b076 influenza c
838	72	4.3	263	2	Q72P38	Q72p38 leptospira	911	72	4.3	641	2	Q8B082	Q8b082 influenza c
839	72	4.3	276	2	Q85MA9	Q85ma9 monoblephar	912	72	4.3	641	2	Q91Q72	Q91q72 influenza c
840	72	4.3	278	2	Q8N7V2	Q8n7v2 homo sapien	913	72	4.3	645	2	Q6CYA8	Q6cyas kluyveromyc
841	72	4.3	279	2	Q640X0	Q640x0 xenopus lae	914	72	4.3	645	2	Q8H241	Q8h241 gossypium h
842	72	4.3	306	2	Q6F9I5	Q6f9i5 acinetobact	915	72	4.3	649	2	Q39661	Q39661 influenza c
843	72	4.3	310	2	Q9M2Y9	Q9m2y9 arabidopsis	916	72	4.3	649	2	Q67416	Q67416 influenza c
844	72	4.3	311	2	Q8CQC9	Q8cq9 staphylococ	917	72	4.3	652	2	Q711P7	Q711p7 leishmania
845	72	4.3	312	2	Q9DPS7	Q9dps7 meleagrid h	918	72	4.3	654	1	HEMA_INCCA	Q711p7 influenza c
846	72	4.3	312	2	Q9E1I3	Q9e1i3 meleagrid h	919	72	4.3	655	1	HEMA_INCUH	P03465 influenza c
847	72	4.3	316	2	Q8PLU9	Q8plu9 xanthomonas	920	72	4.3	655	1	NA10_HUMAN	Q86w26 homo sapien
848	72	4.3	320	2	Q98R15	Q98r15 mycoplasma	921	72	4.3	658	1	Q8EE51	Q8ee51 shewanella
849	72	4.3	328	2	Q83GG6	Q83g96 tropheryma	922	72	4.3	697	2	Q6FAA6	Q6faa6 acinetobact
850	72	4.3	330	2	Q9KA44	Q9ka44 bacillus ha	923	72	4.3	712	2	Q9CISI	Q9ci81 lactococcus
851	72	4.3	342	2	Q96BE4	Q96be4 homo sapien	924	72	4.3	737	2	Q9CISI	Q9dws7 rat cytomeg
852	72	4.3	346	2	P91677	P91677 drosophila	925	72	4.3	751	1	UAS3_DROME	Q9vces drosophila
853	72	4.3	350	2	Q6A0B4	Q6a0b4 mus musculu	926	72	4.3	760	2	Q6ZCS7	Q6zcs7 oryza sativ
854	72	4.3	352	1	COBT_CLOAB	Q97jb4 clostridium	927	72	4.3	768	2	Q9ZS81	Q9z881 lycopersico
855	72	4.3	353	2	Q76LN0	Q76ln0 homo sapien	928	72	4.3	781	2	Q41269	Q41269 spodoptera
856	72	4.3	353	2	Q6AR61	Q6ar61 desulfotale	929	72	4.3	790	2	Q6CSV0	Q6csvo kluyveromyc
857	72	4.3	360	2	O25195	O25195 helicobacte	930	72	4.3	812	2	Q7RJ31	Q7rj31 plasmodium
858	72	4.3	370	1	H181_BACCR	Q81fq1 bacillus ce	931	72	4.3	839	2	Q6P3N7	Q6p3n7 xenopus tro
859	72	4.3	372	2	Q7YSL1	Q7ysl1 culex pipie	932	72	4.3	860	2	Q9FHN0	Q9fhn0 arabidopsis
860	72	4.3	379	1	PATA_ANASP	Q7z0z4 culex pipie	933	72	4.3	882	1	ALKS_PSEOL	P17051 pseudomonas
861	72	4.3	387	1	SUCC_XYLFA	P39048 anabaena sp	934	72	4.3	998	2	Q8ZXL7	Q8zx17 pyrobaculum
862	72	4.3	387	1	SUCC_XYLFT	Q9pah1 xylella fas	935	72	4.3	1038	2	Q6MDY1	Q6mdy1 parachlamyd
863	72	4.3	387	1	SUCC_XYLFT	Q87a98 xylella fas	936	72	4.3	1048	2	Q6FK38	Q6fk38 candida gla
864	72	4.3	396	2	Q6U9K9	Q6u9k9 bacterioph	937	72	4.3	1069	1	S24B_ARATH	Q9m081 arabidopsis
865	72	4.3	416	2	Q7VPS0	Q7vps0 chlamydia p	938	72	4.3	1081	2	Q94LU2	Q94lu2 oryza sativ
866	72	4.3	430	2	Q9JRZ1	Q9jrz1 chlamydia p	939	72	4.3	1114	2	Q717V6	Q717v6 stellaria l
867	72	4.3	430	2	Q9Z6U2	Q9z6u2 chlamydia p	940	72	4.3	1118	2	Q41335	Q41335 lycopersico
868	72	4.3	449	1	GAD_MOUSE	P22933 mus musculu	941	72	4.3	1125	2	Q925C2	Q925c2 mus musculu
869	72	4.3	449	2	Q8VBV6	Q8vbv6 mus musculu	942	72	4.3	1158	2	Q88W93	Q88wn3 pseudomonas
870	72	4.3	450	2	Q9FIA0	Q9fia0 arabidopsis	943	72	4.3	1166	2	Q8RWT2	Q8rwt2 arabidopsis
871	72	4.3	454	2	O65425	O65425 arabidopsis	944	72	4.3	1166	2	Q9LHE9	Q9lhe9 arabidopsis
872	72	4.3	454	2	Q65LN0	Q65ln0 bacillus li	945	72	4.3	1166	2	Q9SNF0	Q9snf0 arabidopsis
873	72	4.3	457	1	FKB5_SAGOB	O9xsi2 saginus oe	946	72	4.3	1177	2	Q6A086	Q6a086 mus musculu
874	72	4.3	457	2	Q8LW9	Q8lwp9 ranodon sib	947	72	4.3	1247	2	Q7PT06	Q7pt06 anopheles g
875	72	4.3	462	2	Q99M97	Q99m97 mus musculu	948	72	4.3	1351	2	Q7PZ23	Q7pz23 anopheles g
876	72	4.3	464	2	Q9FI99	Q9fi99 arabidopsis	949	72	4.3	1411	2	Q6V3V8	Q6v3v8 drosophila
877	72	4.3	470	1	VAH2_CABEL	Q22494 caenorhabdi	950	72	4.3	1411	2	Q9SJ92	Q9sj92 arabidopsis
878	72	4.3	477	2	Q8YYB6	Q8yyb6 neurospora	951	72	4.3	1429	2	O15764	O15764 tetrahymena
879	72	4.3	480	2	Q7SC42	Q7sc42 neurospora	952	72	4.3	1459	1	LHN2_HUMAN	O95490 homo sapien
880	72	4.3	490	2	Q6BP12	Q6bp12 debaryomyce	953	72	4.3	1524	2	Q6CBR1	Q6cbr1 yarrowia li
881	72	4.3	495	2	Q6ESK6	Q6esk6 oryza sativ	954	72	4.3	1583	2	Q8K4P8	Q8k4p8 mus musculu
882	72	4.3	499	2	Q9A9H8	Q9a9h8 caulobacter	955	72	4.3	1589	2	Q9U0Q9	Q9uug9 metarhizium
883	72	4.3	512	2	O56677	O56677 coccal virus	956	72	4.3	1618	2	Q7ZT77	Q7zt77 xenopus lae
884	72	4.3	538	2	Q9JAE2	Q9jae2 mumps virus	957	72	4.3	1664	2	Q6BNP3	Q6bnp3 debaryomyce
885	72	4.3	552	2	Q7UM91	Q7um91 rhodopitrell	958	72	4.3	1784	2	Q9CDB1	Q9cdb1 mycobacteri
886	72	4.3	554	2	Q6GV72	Q6gv72 cikopleura	959	72	4.3	1902	2	Q6FVQ9	Q6fvq9 candida gla
887	72	4.3	600	1	NUCD_ECOLI	P33599 escherichia	960	72	4.3	2006	2	Q7R5W2	Q7r5w2 giardia lam
888	72	4.3	611	1	RBT3_MOUSE	Q9ctn4 mus musculu	961	72	4.3	2073	2	Q6FM66	Q6fm66 homo sapien
889	72	4.3	641	2	Q8QZN7	Q8qzn7 influenza c	962	72	4.3	2104	2	Q6Q883	Q6q883 candida gla
890	72	4.3	641	2	Q8QZN8	Q8qzn8 influenza c	963	72	4.3	2176	2	Q6Q883	Q6q883 leptosphaer
891	72	4.3	641	2	Q8QZN9	Q8qzn9 influenza c	964	72	4.3	2222	2	Q7R4B1	Q7r4b1 giardia lam
892	72	4.3	641	2	Q8QZP0	Q8qzp0 influenza c	965	72	4.3	3011	1	YOS1_SCHPO	P87319 schizosacch
893	72	4.3	641	2	Q8QZP2	Q8qzp2 influenza c	966	72	4.3	3088	2	Q9WID3	Q9wid3 chilli vein
894	72	4.3	641	2	Q68CF0	Q68cf0 influenza c	967	72	4.3	4533	2	Q9BIX3	Q9bix3 tetrahymena
895	72	4.3	641	2	Q68CF2	Q68cf2 influenza c	968	71.5	4.2	135	2	Q18158	Q18158 caenorhabdi
896	72	4.3	641	2	Q68CF3	Q68cf3 influenza c	969	71.5	4.2	173	2	Q9XUA4	Q9xua4 caenorhabdi
897	72	4.3	641	2	Q68CF4	Q68cf4 influenza c	970	71.5	4.2	205	2	Q9NPM7	Q9npt7 homo sapien
898	72	4.3	641	2	Q68CF7	Q68cf7 influenza c	971	71.5	4.2	222	1	UPAS_MOUSE	P35457 mus musculu
899	72	4.3	641	2	Q68CF9	Q68cf9 influenza c	972	71.5	4.2	231	2	Q7SYN9	Q7syn9 xenopus lae
900	72	4.3	641	2	Q68CG0	Q68cg0 influenza c	973	71.5	4.2	232	2	Q6QRL6	Q6qrl6 eurycea tym
901	72	4.3	641	2	Q68CG2	Q68cg2 influenza c	974	71.5	4.2	261	2	Q46277	Q46277 chlamydia p
902	72	4.3	641	2	Q68CG3	Q68cg3 influenza c	975	71.5	4.2	296	1	COPE_YEAST	P40509 saccharomyc
903	72	4.3	641	2	Q68CG5	Q68cg5 influenza c	976	71.5	4.2	297	1	PSD_PHOLT	Q7my86 photorhabdu
904	72	4.3	641	2	Q68CG6	Q68cg6 influenza c	977	71.5	4.2	306	2	Q8ED96	Q8ed96 shewanella
905	72	4.3	641	2	Q68CG7	Q68cg7 influenza c	978	71.5	4.2	309	2	Q62T73	Q62t73 bacillus li
906	72	4.3	641	2	Q8B069	Q8b069 influenza c	979	71.5	4.2	318	2	Q65E14	Q65e14 bacillus li
907	72	4.3	641	2	Q8B070	Q8b070 influenza c	980	71.5	4.2	322	1	PSD_ECOLI	P10740 escherichia

981	71.5	4.2	326	2	Q8JHW3	Q8jhw3 xenopus lae
982	71.5	4.2	338	2	Q8JH92	Q8jh92 xenopus lae
983	71.5	4.2	338	2	Q6DFA7	Q6dfa7 xenopus lae
984	71.5	4.2	340	2	Q81PY9	Q81py9 bacillus an
985	71.5	4.2	340	2	Q6H167	Q6h167 bacillus th
986	71.5	4.2	346	2	Q9ZFW7	Q9zfw7 pseudomonas
987	71.5	4.2	353	2	Q6ZOV7	Q6zov7 oryza sativ
988	71.5	4.2	357	2	Q8R112	Q8r112 mus musculu
989	71.5	4.2	359	1	WECF_ECO57	Q8xaq8 escherichia
990	71.5	4.2	359	1	WECF_ECOL6	Q8f1bp9 escherichia
991	71.5	4.2	359	2	Q6FMP2	Q6fmp2 candida gla
992	71.5	4.2	362	2	Q22486	Q22486 oryza sativ
993	71.5	4.2	378	2	Q62012	Q62012 caenorhabdi
994	71.5	4.2	379	2	Q9XNX8	Q9xnx8 akodon nigr
995	71.5	4.2	380	2	Q66SS6	Q66ss6 geocalamus
996	71.5	4.2	394	2	Q745Y2	Q745y2 thermus the
997	71.5	4.2	400	2	Q9GZH7	Q9gzh7 caenorhabdi
998	71.5	4.2	412	2	Q9P9X9	Q9p9x9 xylella fas
999	71.5	4.2	421	1	TEG3_MAIZE	Q41874 zea mays (m
1000	71.5	4.2	424	2	Q9PLH9	Q9plh9 chlamydia m
1001	71.5	4.2	428	1	RF4_KLULA	P09806 kluyveromyc
1002	71.5	4.2	453	2	Q06671	Q06671 saccharomyc
1003	71.5	4.2	457	2	Q644G9	Q644g9 gyrinophilu
1004	71.5	4.2	493	2	Q73N78	Q73n78 treponema d
1005	71.5	4.2	519	2	Q8C249	Q8c249 m mus muscu
1006	71.5	4.2	520	2	Q8MNU4	Q8mnj4 dictyosteli
1007	71.5	4.2	563	2	Q751M3	Q751m3 ashbya goss
1008	71.5	4.2	567	2	Q8XI66	Q8xi66 clostridium
1009	71.5	4.2	569	2	Q9W250	Q9w250 drosophila
1010	71.5	4.2	585	2	Q8UVV3	Q8uvv3 brachydanio
1011	71.5	4.2	590	2	Q9FNN8	Q9fnn8 arabidopsis
1012	71.5	4.2	598	2	Q9LVS1	Q9lvs1 arabidopsis
1013	71.5	4.2	601	2	Q6PGV3	Q6pgv3 brachydanio
1014	71.5	4.2	601	2	Q7ZWL2	Q7zwl2 xenopus lae
1015	71.5	4.2	621	2	Q66708	Q66708 aquifex aeo
1016	71.5	4.2	632	2	Q8AUT3	Q8aut3 brachydanio
1017	71.5	4.2	658	1	SYM_ARCFU	Q28819 archaeoglob
1018	71.5	4.2	664	2	Q7OX73	Q7gx73 giardia lam
1019	71.5	4.2	672	2	Q9FQ93	Q9fq93 nicotiana t
1020	71.5	4.2	679	2	Q6FY73	Q6fy73 candida gla
1021	71.5	4.2	691	1	VP33_YEAST	P20795 saccharomyc
1022	71.5	4.2	725	2	Q98TA2	Q98ta2 brachydanio
1023	71.5	4.2	725	2	Q8AYH1	Q8ayh1 brachydanio
1024	71.5	4.2	736	2	Q9VKQ7	Q9vkq7 drosophila
1025	71.5	4.2	737	2	Q8JZM4	Q8jzm4 mus musculu
1026	71.5	4.2	737	2	Q8R4T6	Q8r4t6 mus musculu
1027	71.5	4.2	737	2	Q8VD97	Q8vd97 mus musculu
1028	71.5	4.2	745	2	Q9FX37	Q9fx37 arabidopsis
1029	71.5	4.2	751	2	Q01497	Q01497 caenorhabdi
1030	71.5	4.2	773	2	Q9VQR1	Q9vqr1 drosophila
1031	71.5	4.2	796	1	PTRA_RAT	Q03348 rattus norv
1032	71.5	4.2	815	2	Q19107	Q19107 caenorhabdi
1033	71.5	4.2	822	2	Q7QWB9	Q7qwb9 giardia lam
1034	71.5	4.2	825	2	Q6FXE2	Q6fxe2 candida gla
1035	71.5	4.2	861	2	Q9XWF9	Q9xwf9 caenorhabdi
1036	71.5	4.2	874	2	Q7S1P9	Q7s1p9 chimpanzee
1037	71.5	4.2	908	2	Q86J00	Q86j00 dictyosteli
1038	71.5	4.2	975	2	Q80W30	Q80w30 mus musculu
1039	71.5	4.2	985	2	Q80W52	Q80w52 mus musculu
1040	71.5	4.2	1004	2	Q6XUG7	Q6xjg7 arabidopsis
1041	71.5	4.2	1056	1	RIC1_YEAST	P40395 saccharomyc
1042	71.5	4.2	1063	1	PDR1_YEAST	P12383 saccharomyc
1043	71.5	4.2	1063	2	Q8SR27	Q8sr27 encephalito
1044	71.5	4.2	1067	2	Q7SHQ9	Q7shq9 neurospora
1045	71.5	4.2	1079	2	Q9HE48	Q9he48 neurospora
1046	71.5	4.2	1086	2	Q9TYN3	Q9tyn3 caenorhabdi
1047	71.5	4.2	1115	2	Q8CBC1	Q8cbc1 mus musculu
1048	71.5	4.2	1142	2	Q751X9	Q751x9 ashbya goss
1049	71.5	4.2	1256	2	Q6LU92	Q6lu92 photobacter
1050	71.5	4.2	1315	2	Q8CBA9	Q8cba9 mus musculu
1051	71.5	4.2	1450	2	Q8A097	Q8a097 bacteroides
1052	71.5	4.2	1508	2	Q80WMO	Q80wmo mus musculu
1053	71.5	4.2	1558	2	Q6P4I6	Q6p4i6 mus musculu
1054	71.5	4.2	1627	2	Q84ZL0	Q84zl0 oryza sativ
1055	71.5	4.2	1712	2	Q81Y21	Q81y21 homo sapien
1056	71.5	4.2	1744	2	Q8CHH1	Q8chh1 mus musculu
1057	71.5	4.2	1896	2	Q6FV91	Q6fv91 candida gla
1058	71.5	4.2	1916	2	Q75AF0	Q75af0 ashbya goss
1059	71.5	4.2	2013	2	Q6PHU4	Q6phu4 mus musculu
1060	71.5	4.2	2273	2	Q86AJ5	Q86aj5 dictyosteli
1061	71.5	4.2	2427	2	Q80SU7	Q80su7 mus musculu
1062	71.5	4.2	2567	2	Q9U0J6	Q9u0j6 plasmodium
1063	71.5	4.2	2715	1	MLL4_HUMAN	Q9umt6 homo sapien
1064	71.5	4.2	2867	2	Q8YEPI	Q8yep1 brucella me
1065	71.5	4.2	3056	2	Q6Y1D8	Q6y1d8 bean yellow
1066	71.5	4.2	3075	2	Q8AW10	Q8aw10 brachydanio
1067	71	4.2	144	2	Q6RC42	Q6rc42 drosophila
1068	71	4.2	198	2	Q8YZE9	Q8yze9 anabaena sp
1069	71	4.2	200	2	Q6DIV3	Q6div3 xenopus tro
1070	71	4.2	220	2	Q20008	Q20008 caenorhabdi
1071	71	4.2	234	1	LUXG_PHOLE	P29237 photobacter
1072	71	4.2	256	1	NDBE_PIG	P01214 sus scrofa
1073	71	4.2	257	2	Q9C9Q0	Q9c9q0 arabidopsis
1074	71	4.2	262	2	Q9JMF0	Q9jmf0 mus musculu
1075	71	4.2	291	2	Q7XYL6	Q7xy16 chlorarachn
1076	71	4.2	307	2	Q24344	Q24344 sorghum bic
1077	71	4.2	327	1	SIN4_ARATH	Q9stn8 arabidopsis
1078	71	4.2	331	1	RBSR_HAEIN	P44329 haemophilus
1079	71	4.2	336	1	Q6CUP5	Q6cup5 kluyveromyc
1080	71	4.2	366	2	TORY_ECO57	P58361 escherichia
1081	71	4.2	375	2	Q8AXN2	Q8axn2 xenopus lae
1082	71	4.2	388	2	Q8NEU7	Q8neu7 homo sapien
1083	71	4.2	390	2	Q9FZR6	Q9fzr6 mycoplasma
1084	71	4.2	390	2	Q7NZ47	Q7nz47 chromobacte
1085	71	4.2	399	2	Q86YH6	Q86yh6 homo sapien
1086	71	4.2	399	2	Q9NR58	Q9nr58 homo sapien
1087	71	4.2	410	1	GC5B_MOUSE	Q92320 mus musculu
1088	71	4.2	413	2	Q6CLA9	Q6cla9 kluyveromyc
1089	71	4.2	420	2	Q6ZAJ8	Q6zaj8 oryza sativ
1090	71	4.2	441	2	Q8D384	Q8d384 wiggleswort
1091	71	4.2	455	2	Q43168	Q43168 solanum tub
1092	71	4.2	464	2	Q7VLH5	Q7vlh5 haemophilus
1093	71	4.2	475	2	Q8ELI8	Q8elj8 oceanobacil
1094	71	4.2	487	2	Q6C1J3	Q6c1j3 kluyveromyc
1095	71	4.2	491	2	Q8EHY2	Q8ehy2 shewanella
1096	71	4.2	511	1	HUTH_VIBCH	Q9ksg4 vibrio chol
1097	71	4.2	511	2	Q84AQ2	Q84aq2 pseudomonas
1098	71	4.2	538	2	Q6EAM3	Q6eam3 mumps virus
1099	71	4.2	566	1	SNFC_YEAST	P53628 saccharomyc
1100	71	4.2	572	2	Q7S3D6	Q7s3d6 neurospora
1101	71	4.2	589	2	Q8LQG2	Q8lqg2 oryza sativ
1102	71	4.2	589	2	Q9LWZ0	Q9lwz0 oryza sativ
1103	71	4.2	592	2	Q8FMD8	Q8fmd8 corynebacte
1104	71	4.2	600	2	Q8FEJ7	Q8ffj7 escherichia
1105	71	4.2	600	2	Q8XCW9	Q8xcw9 escherichia
1106	71	4.2	601	2	Q8AQSF	Q8aqsf shigella fl
1107	71	4.2	608	2	Q993G8	Q993g8 callitrichi
1108	71	4.2	626	2	Q782R2	Q782r2 gallid herp
1109	71	4.2	626	2	Q9WSY1	Q9wsy1 marek's dis
1110	71	4.2	634	2	Q7KX02	Q7kx02 caenorhabdi
1111	71	4.2	637	2	Q6LR72	Q6lr72 photobacter
1112	71	4.2	640	2	Q8QZM6	Q8qzm6 influenza c
1113	71	4.2	640	2	Q8QZM7	Q8qzm7 influenza c
1114	71	4.2	640	2	Q8QZM8	Q8qzm8 influenza c
1115	71	4.2	640	2	Q8QZM9	Q8qzm9 influenza c
1116	71	4.2	640	2	Q8QZN0	Q8qzn0 influenza c
1117	71	4.2	640	2	Q8QZN3	Q8qzn3 influenza c
1118	71	4.2	640	2	Q8QZN4	Q8qzn4 influenza c
1119	71	4.2	640	2	Q8QZN5	Q8qzn5 influenza c
1120	71	4.2	640	2	Q8QZN6	Q8qzn6 influenza c
1121	71	4.2	640	2	Q68CF6	Q68cf6 influenza c
1122	71	4.2	640	2	Q68CG4	Q68cg4 influenza c
1123	71	4.2	641	1	HEMA_INCKY	P17003 influenza c
1124	71	4.2	641	1	HEMA_INCHY	P17003 influenza c
1125	71	4.2	641	1	HEMA_INCKY	P17003 influenza c
1126	71	4.2	641	1	HEMA_INCNCA	P17005 influenza c

1127	71	4.2	641	2	Q8QZP1	Q8qzpi	influenza c	1200	70.5	4.2	397	2	Q6LN30	Q6ln30	photobacter
1128	71	4.2	641	2	Q8B073	Q8b073	influenza c	1201	70.5	4.2	411	2	Q9A3L1	Q9a3l1	caulobacter
1129	71	4.2	645	2	Q8B075	Q8b075	influenza c	1202	70.5	4.2	429	1	THRC_SERMA	P27735	serattia ma
1130	71	4.2	645	2	Q9IQ68	Q9iq68	influenza c	1203	70.5	4.2	438	2	Q90ZM7	Q90zm7	petromyzon
1131	71	4.2	650	2	Q9IL54	Q9il54	oryza sativ	1204	70.5	4.2	451	2	Q8N6V2	Q8n6v2	homo sapien
1132	71	4.2	662	1	APTX_DROME	Q8msg8	drosophila	1205	70.5	4.2	451	2	Q9LKG8	Q9lkg8	arabidopsis
1133	71	4.2	665	2	Q9N2V0	Q9n2v0	caenorhabdi	1206	70.5	4.2	452	2	Q9YH86	Q9yh86	gallus gall
1134	71	4.2	668	2	Q6NRG6	Q6nrg6	xenopus lae	1207	70.5	4.2	458	2	Q8HS0	Q8hs0	dictyosteli
1135	71	4.2	669	1	NAH6_HUMAN	Q92581	homo sapien	1208	70.5	4.2	460	2	Q94SE6	Q94se6	mastacemba
1136	71	4.2	669	2	Q93ZA2	Q93za2	arabidopsis	1209	70.5	4.2	464	2	Q9W212	Q9w212	drosophila
1137	71	4.2	683	2	Q7XXL3	Q7xxl3	oryza sativ	1210	70.5	4.2	469	1	TBGT_MAIZE	Q41808	zea mays (m
1138	71	4.2	701	2	Q86VS0	Q86vs0	homo sapien	1211	70.5	4.2	472	1	ET2B_XENLA	Q91712	xenopus lae
1139	71	4.2	715	2	Q7NOY6	Q7noy6	photorhabdu	1212	70.5	4.2	472	2	Q8GZT0	Q8gztc	lupinus alb
1140	71	4.2	721	2	Q87MU6	Q87mu6	vibrio para	1213	70.5	4.2	472	2	Q6DE76	Q6de76	xenopus lae
1141	71	4.2	728	1	ANC2_CAEEL	P34514	caenorhabdi	1214	70.5	4.2	474	1	TBGT_ARATH	P38558	arabidopsis
1142	71	4.2	731	2	Q7ZXU8	Q7zxu8	xenopus lae	1215	70.5	4.2	475	2	Q7XJCI	Q7xjci	haplomitriu
1143	71	4.2	735	2	Q9VP12	Q9vp12	drosophila	1216	70.5	4.2	479	2	Q8CTE4	Q8cte4	etaphylococ
1144	71	4.2	749	2	Q9NC88	Q9nc88	strongyloce	1217	70.5	4.2	496	2	Q9Z790	Q9z790	chlamydia p
1145	71	4.2	751	1	PHYB_ANASP	Q9r6x3	anabaena sp	1218	70.5	4.2	517	2	Q9CFN1	Q9cfn1	lactococcus
1146	71	4.2	765	1	METE_LISMO	Q8y6k3	listeria mo	1219	70.5	4.2	540	2	Q7TIM6	Q7tim6	silurus mer
1147	71	4.2	774	2	Q8RP17	Q8rp17	pseudomonas	1220	70.5	4.2	547	2	Q9ILR9	Q9ilr9	artemisia a
1148	71	4.2	776	2	Q9C8H3	Q9c8h3	arabidopsis	1221	70.5	4.2	547	2	Q9ST45	Q9st45	artemisia a
1149	71	4.2	784	2	Q7U6Y4	Q7u6y4	synecococc	1222	70.5	4.2	557	2	Q7R3Y2	Q7r3y2	glardia lam
1150	71	4.2	794	2	Q9V5N6	Q9v5n6	drosophila	1223	70.5	4.2	592	2	Q834P9	Q834p9	enterococcu
1151	71	4.2	794	2	Q9FL59	Q9fl59	arabidopsis	1224	70.5	4.2	601	2	Q68975	Q68975	versinia en
1152	71	4.2	826	2	Q6C381	Q6c381	yarrowia li	1225	70.5	4.2	605	2	ALS_HUMAN	P35858	homo sapien
1153	71	4.2	836	1	POSN_HUMAN	Q43393	brassica na	1226	70.5	4.2	605	2	Q8TAX0	Q8tax0	homo sapien
1154	71	4.2	849	2	Q43393	Q43393	homo sapien	1227	70.5	4.2	623	2	Q6TIS6	Q6tis6	homo sapien
1155	71	4.2	850	2	Q6MZW3	Q6mzw3	homo sapien	1228	70.5	4.2	626	2	Q7PNH3	Q7pnh3	anopheles g
1156	71	4.2	891	1	LHN2_MOUSE	Q8jzz7	mus musculu	1229	70.5	4.2	628	2	Q6MHW0	Q6mhw0	bdeiliovibri
1157	71	4.2	943	2	Q7A8N8	Q7a8n8	escherichia	1230	70.5	4.2	630	2	Q95Y88	Q95y88	caenorhabdi
1158	71	4.2	944	2	Q6DCL5	Q6dcl5	xenopus lae	1231	70.5	4.2	634	2	Q74879	Q74879	schizosacch
1159	71	4.2	951	2	Q9HTC4	Q9htc4	pseudomonas	1232	70.5	4.2	662	2	Q8YML4	Q8yml4	anabaena sp
1160	71	4.2	952	2	Q8XC73	Q8xc73	escherichia	1233	70.5	4.2	665	1	RNR2_LACIA	Q02146	lactococcus
1161	71	4.2	963	2	Q8V9U2	Q8v9u2	african swi	1234	70.5	4.2	680	1	KALM_HUMAN	P23352	homo sapien
1162	71	4.2	967	2	Q6SYZ9	Q6syz9	streptococc	1235	70.5	4.2	697	2	Q9LUI6	Q9lui6	arabidopsis
1163	71	4.2	980	2	Q7QOV6	Q7qov6	glardia lam	1236	70.5	4.2	708	2	Q6P9I3	Q6p9i3	xenopus lae
1164	71	4.2	992	2	Q7KTV9	Q7ktv9	drosophila	1237	70.5	4.2	712	2	Q6P4W3	Q6p4w3	xenopus tro
1165	71	4.2	1024	2	Q8A2X6	Q8a2x6	bacteroides	1238	70.5	4.2	715	1	YME1_MOUSE	Q88967	mus musculu
1166	71	4.2	1093	2	Q6MF79	Q6mf79	parachlamyd	1239	70.5	4.2	717	2	O043Z5	O043z5	arabidopsis
1167	71	4.2	1180	2	Q751H7	Q751h7	ashbya goss	1240	70.5	4.2	735	2	O51543	O51543	borrelia bu
1168	71	4.2	1219	2	Q7G7H3	Q7g7h3	oryza sativ	1241	70.5	4.2	770	2	Q72J77	Q72j77	thermus the
1169	71	4.2	1219	2	Q9AY59	Q9ay59	oryza sativ	1242	70.5	4.2	786	2	Q6CC33	Q6cc33	yarrowia li
1170	71	4.2	1240	2	Q9T0B7	Q9t0b7	arabidopsis	1243	70.5	4.2	801	2	Q7XKV0	Q7xkv0	oryza sativ
1171	71	4.2	1453	2	Q94KV0	Q94kv0	arabidopsis	1244	70.5	4.2	816	2	Q6FV19	Q6fv19	candida gla
1172	71	4.2	1453	2	Q9C6F9	Q9c6f9	arabidopsis	1245	70.5	4.2	855	2	Q86Y56	Q86y56	homo sapien
1173	71	4.2	1485	2	Q80TZ5	Q80tz5	mus musculu	1246	70.5	4.2	877	2	Q6K297	Q6k297	oryza sativ
1174	71	4.2	1504	2	Q9LKU4	Q9lk4	arabidopsis	1247	70.5	4.2	893	2	O53121	O53121	mycobacteri
1175	71	4.2	1535	2	Q7RKI1	Q7rk11	plasmodium	1248	70.5	4.2	901	2	Q9LRA3	Q9lra3	arabidopsis
1176	71	4.2	2109	2	Q8B0H0	Q8b0h0	vesicular s	1249	70.5	4.2	905	2	Q8T655	Q8t655	dirofilaria
1177	71	4.2	2169	2	Q7R3M1	Q7r3m1	glardia lam	1250	70.5	4.2	911	2	Q68KF9	Q68kf9	xenopus lae
1178	71	4.2	2842	1	APC_RAT	P70478	rattus norv	1251	70.5	4.2	914	2	Q6N3P3	Q6n3p3	rhodopseudo
1179	71	4.2	3122	2	Q8B3T9	Q8b3t9	citrus tris	1252	70.5	4.2	935	2	Q750Y5	Q750y5	ashbya goss
1180	71	4.2	3124	2	Q66237	Q66237	citrus tris	1253	70.5	4.2	937	2	Q8CDG6	Q8cdg6	mus musculu
1181	71	4.2	3403	2	Q7T5A6	Q7t5a6	onion. yello	1254	70.5	4.2	937	2	Q9D5Y1	Q9d5y1	mus musculu
1182	71	4.2	4717	2	Q94248	Q94248	schizosacch	1255	70.5	4.2	944	1	VP35_YEAST	P34110	saccharomyc
1183	70.5	4.2	152	2	Q92AR5	Q92ar5	listeria in	1256	70.5	4.2	991	2	Q941F4	Q941f4	arabidopsis
1184	70.5	4.2	186	2	Q72LV6	Q72lv6	leptospira	1257	70.5	4.2	995	2	Q9ZVM2	Q9zvm2	arabidopsis
1185	70.5	4.2	232	2	Q6QRH8	Q6qtrh8	eurycea tyr	1258	70.5	4.2	1009	2	Q9M295	Q9m295	arabidopsis
1186	70.5	4.2	241	2	Q8SFK2	Q8sfk2	oryzomya pa	1259	70.5	4.2	1031	2	Q8OU53	Q8ou53	mus musculu
1187	70.5	4.2	242	2	Q9Y1P9	Q9y1p9	pseudoposte	1260	70.5	4.2	1035	2	Q6Y7W7	Q6y7w7	homo sapien
1188	70.5	4.2	246	2	Q89ZC2	Q89zc2	bacteroides	1261	70.5	4.2	1061	2	Q7T184	Q7t184	xenopus lae
1189	70.5	4.2	251	2	Q64XE3	Q64xe3	bacteroides	1262	70.5	4.2	1061	2	Q640I8	Q640i8	xenopus lae
1190	70.5	4.2	276	2	Q81EN6	Q81en6	bacillus ce	1263	70.5	4.2	1086	2	O18887	O18887	sus scrofa
1191	70.5	4.2	284	2	Q90Y00	Q90y00	petromyzon	1264	70.5	4.2	1123	2	Q8ZMB4	Q8zmb4	salmonella
1192	70.5	4.2	288	2	Q8EEL1	Q8eel1	shewanella	1265	70.5	4.2	1132	2	Q9SFG5	Q9sfgs	arabidopsis
1193	70.5	4.2	308	2	Q6LS59	Q6l859	photobacter	1266	70.5	4.2	1136	1	C4BA_BACTI	P05519	bacillus th
1194	70.5	4.2	334	2	O17053	O17053	caenorhabdi	1267	70.5	4.2	1142	1	GLG1_CHICK	Q02391	gallus gall
1195	70.5	4.2	351	2	Q7SE34	Q7se34	neurospora	1268	70.5	4.2	1147	2	Q7Q642	Q7q642	anopheles g
1196	70.5	4.2	370	2	Q8EE52	Q8ee52	shewanella	1269	70.5	4.2	1180	1	C4AA_BACTI	P16480	bacillus th
1197	70.5	4.2	391	2	Q9FNN0	Q9fn0	arabidopsis	1270	70.5	4.2	1180	2	Q6PB43	Q6pb43	mus musculu
1198	70.5	4.2	392	2	Q9N2S1	Q9n2s1	caenorhabdi	1271	70.5	4.2	1193	1	SPAS_HUMAN	Q96r06	homo sapien
1199	70.5	4.2	395	2	P91419	P91419	caenorhabdi	1272	70.5	4.2	1279	2	O26046	O26046	helicobacte

1273	70.5	4.2	1356	2	Q9GQ90	Q9gq90 dirofilaria	1346	70	4.1	538	2	Q9DQA2	Q9dqa2 mumps virus
1274	70.5	4.2	1370	1	Z261_MOUSE	Q9jlm4 mus musculu	1347	70	4.1	538	2	Q9JAE4	Q9jae4 mumps virus
1275	70.5	4.2	1529	2	Q67VK5	Q67vk5 oryza sativ	1348	70	4.1	552	2	Q72728	Q72728 cucurbit ye
1276	70.5	4.2	1553	2	Q96452	Q96452 nossema locu	1349	70	4.1	557	2	Q8RZ75	Q8rz75 oryza sativ
1277	70.5	4.2	1770	2	Q07791	Q07791 saccharomyc	1350	70	4.1	569	2	Q21837	Q21837 caenorhabdi
1278	70.5	4.2	1805	1	HMW2_MYCGB	P47460 mycoplasma	1351	70	4.1	575	2	Q9H6R5	Q9h6r5 homo sapien
1279	70.5	4.2	1878	2	Q9SYJ7	Q9syj7 arabidopsis	1352	70	4.1	575	2	Q67MU2	Q67mu2 symbiobacte
1280	70.5	4.2	1942	2	Q23450	Q23450 arabidopsis	1353	70	4.1	577	2	Q6GM80	Q6gm80 xenopus lae
1281	70.5	4.2	2233	2	Q94711	Q94711 paramecium	1354	70	4.1	578	1	CIDD_SCHPO	Q9ut49 schizosacch
1282	70.5	4.2	2238	1	GOA4_MOUSE	Q91vw5 mus musculu	1355	70	4.1	585	2	Q9M255	Q9m255 arabidopsis
1283	70.5	4.2	2443	2	Q96J17	Q96j17 homo sapien	1356	70	4.1	608	2	Q9M256	Q9m256 arabidopsis
1284	70.5	4.2	2603	2	Q869W9	Q869w9 dictyosteli	1357	70	4.1	609	2	Q82670	Q82670 influenza c
1285	70.5	4.2	2843	1	APC_HUMAN	P25054 homo sapien	1358	70	4.1	609	2	Q82671	Q82671 influenza c
1286	70.5	4.2	3329	1	BRC2_MOUSE	P97929 mus musculu	1359	70	4.1	619	2	Q82675	Q82675 influenza c
1287	70.5	4.2	3329	2	Q8VHD0	Q8vhd0 mus musculu	1360	70	4.1	619	2	Q754B0	Q754e0 ashbya goss
1288	70.5	4.2	3868	2	Q9W090	Q9w090 drosophila	1361	70	4.1	625	2	Q7S319	Q7s319 neurospora
1289	70.5	4.2	3966	2	Q7KVA7	Q7kva7 drosophila	1362	70	4.1	633	2	Q9V6C5	Q9v6c5 drosophila
1290	70.5	4.2	5120	1	PCLO_CHICK	Q9pu36 gallus gall	1363	70	4.1	633	2	Q9CN49	Q9cn49 pasteurella
1291	70.5	4.2	8407	2	Q7RTM4	Q7rtm4 homo sapien	1364	70	4.1	640	2	Q8QZN2	Q8qzn2 influenza c
1292	70	4.1	138	2	Q9LDB3	Q9ldb3 oryza sativ	1365	70	4.1	640	2	Q9Q206	Q9q206 influenza c
1293	70	4.1	144	2	Q6RC43	Q6rc43 drosophila	1366	70	4.1	642	1	HEMA_INCYA	P07969 influenza c
1294	70	4.1	191	2	Q66CM3	Q66cm3 yersinia ps	1367	70	4.1	655	2	Q7R3F3	Q7r3f3 giardia lam
1295	70	4.1	191	2	Q8ZGE7	Q8zge7 yersinia pe	1368	70	4.1	665	1	Y176_METTH	Q26278 methanobact
1296	70	4.1	200	2	Q81308	Q81308 arabidopsis	1369	70	4.1	718	2	Q9B107	Q9b107 entamoeba h
1297	70	4.1	243	2	Q9SMY0	Q9smY0 vltis vinif	1370	70	4.1	727	2	Q9T0B4	Q9t0b4 arabidopsis
1298	70	4.1	244	2	Q9SM95	Q9sm95 oryza sativ	1371	70	4.1	737	2	Q7PNF5	Q7pnf5 anopheles g
1299	70	4.1	247	2	Q9HT53	Q9ht53 pseudomonas	1372	70	4.1	739	2	Q8RCT2	Q8rcu2 pseudomonas
1300	70	4.1	254	2	Q9M6K4	Q9m6k4 oryza sativ	1373	70	4.1	767	2	Q8QS24	Q8qs24 pongine her
1301	70	4.1	256	2	Q9PMW7	Q9pmw7 campylobact	1374	70	4.1	770	2	Q22988	Q22988 arabidopsis
1302	70	4.1	260	2	Q8DVQ5	Q8dvq5 streptococc	1375	70	4.1	772	2	Q6T286	Q6t286 populus alb
1303	70	4.1	265	2	Q9C2G8	Q9c2g8 neurospora	1376	70	4.1	835	1	RP13_ARATH	Q9m67 arabidopsis
1304	70	4.1	269	1	YHT4_YEAST	P38838 saccharomyc	1377	70	4.1	840	2	Q9VZF2	Q9vzf2 drosophila
1305	70	4.1	271	2	Q9SUT9	Q9sut9 arabidopsis	1378	70	4.1	887	2	Q6FQF0	Q6fqf0 candida gla
1306	70	4.1	271	2	Q7YXK5	Q7vyk5 bordetella	1379	70	4.1	888	1	EOL1_ARATH	Q9zqx6 arabidopsis
1307	70	4.1	271	2	Q7WII0	Q7wii0 bordetella	1380	70	4.1	909	2	Q8BX2	Q8bx2 mus musculu
1308	70	4.1	275	2	Q9KTC3	Q9ktc3 vibrio chol	1381	70	4.1	938	2	Q9N4C5	Q9n4c5 caenorhabdi
1309	70	4.1	279	2	Q7ZZ42	Q7zz42 brachydanio	1382	70	4.1	962	1	SUUR_DROME	Q9vce2 drosophila
1310	70	4.1	280	2	Q9YCP1	Q9ycp1 aeropyrum p	1383	70	4.1	964	2	Q72DI8	Q72di8 desulfovibr
1311	70	4.1	293	2	Q6G6Z2	Q6g6z2 staphylococ	1384	70	4.1	971	2	Q6GMY9	Q6gmy9 xenopus lae
1312	70	4.1	308	2	Q8CU92	Q8cu92 staphylococ	1385	70	4.1	978	2	Q6ZU14	Q6zu14 homo sapien
1313	70	4.1	309	2	Q7UMX8	Q7umx8 rhodopirell	1386	70	4.1	1012	2	Q6ZU21	Q6zu21 homo sapien
1314	70	4.1	321	2	Q6UR64	Q6ur64 yersinia fr	1387	70	4.1	1017	2	Q8T391	Q8t391 drosophila
1315	70	4.1	326	2	Q8V707	Q8v707 bovine rota	1388	70	4.1	1029	2	Q9C099	Q9c099 homo sapien
1316	70	4.1	326	2	Q9QTF9	Q9qtf9 human rotav	1389	70	4.1	1037	2	Q6RGL7	Q6g113 xenopus tro
1317	70	4.1	328	2	Q8VU06	Q8vu06 streptococc	1390	70	4.1	1081	2	Q7RFQ3	Q7rfq3 plasmodium
1318	70	4.1	328	2	Q9WYJ0	Q9wyj0 thermotoga	1391	70	4.1	1083	2	Q68FN1	Q68fn1 mus musculu
1319	70	4.1	335	2	Q6BK54	Q6bk54 debaryomyce	1392	70	4.1	1085	1	S124_RAT	Q63632 rattus norv
1320	70	4.1	342	1	HRC4_COREF	Q8fnf4 corynebacte	1393	70	4.1	1143	2	Q6MF84	Q6mf84 parachlamyd
1321	70	4.1	359	2	Q733U3	Q733u3 bacillus ce	1394	70	4.1	1178	2	Q55693	Q55693 synechocyst
1322	70	4.1	366	2	Q7UAC2	Q7uac2 shigella fl	1395	70	4.1	1207	1	GAP2_CABEL	Q8ml25 caenorhabdi
1323	70	4.1	367	2	Q6IX33	Q6ix33 hypholoma f	1396	70	4.1	1222	2	Q8K048	Q8k048 mus musculu
1324	70	4.1	373	2	Q8PDW8	Q8pdw8 xylella fas	1397	70	4.1	1248	2	Q8CH96	Q8ch96 mus musculu
1325	70	4.1	373	2	Q9PDR6	Q9pdr6 xylella fas	1398	70	4.1	1249	2	Q8BS54	Q8bs54 mus musculu
1326	70	4.1	383	2	Q6FX16	Q6fx16 candida gla	1399	70	4.1	1252	2	Q75WU7	Q75wu7 mus musculu
1327	70	4.1	389	2	Q6CK37	Q6ck37 kluyveromyc	1400	70	4.1	1322	2	Q81490	Q81490 arabidopsis
1328	70	4.1	391	2	Q6BFP7	Q6bfp7 paramecium	1401	70	4.1	1358	1	SIR4_YEAST	Q81490 arabidopsis
1329	70	4.1	397	2	Q7URL9	Q7url9 rhodopirell	1402	70	4.1	1409	1	COP1_DROME	P11978 saccharomyc
1330	70	4.1	401	2	Q7RB52	Q7rb52 plasmodium	1403	70	4.1	1409	2	Q08461	P04146 drosophila
1331	70	4.1	411	2	Q23351	Q23351 caenorhabdi	1404	70	4.1	1482	2	Q8GSC4	Q8gsc4 nicotiana t
1332	70	4.1	425	2	Q8LQAS	Q8lqas oryza sativ	1405	70	4.1	1557	2	Q6P405	Q6p405 brachydanio
1333	70	4.1	449	1	GAD_RAT	P18506 rattus norv	1406	70	4.1	1748	1	YNR2_YEAST	P53886 saccharomyc
1334	70	4.1	462	1	TBGI_EUPCR	P54403 euplotes cr	1407	70	4.1	1963	2	Q20641	Q20641 caenorhabdi
1335	70	4.1	468	1	COO6_HUMAN	Q9y2z9 homo sapien	1408	70	4.1	1966	2	Q9SZW8	Q9szw8 arabidopsis
1336	70	4.1	468	2	Q7ULZ5	Q7ulz5 rhodopirell	1409	70	4.1	2052	1	MY10_BOVIN	P79114 bos taurus
1337	70	4.1	472	2	Q9BKU0	Q9bku0 caenorhabdi	1410	70	4.1	2052	1	URRB_SCHPO	O13731 schizosacch
1338	70	4.1	478	2	Q7RFZ2	Q7rfz2 plasmodium	1411	70	4.1	2196	1	MOR2_YEAST	P35194 saccharomyc
1339	70	4.1	485	2	Q86TD4	Q86td4 homo sapien	1412	70	4.1	2493	1	YBA4_MOUSE	Q01705 mus musculu
1340	70	4.1	486	2	Q82044	Q82044 human rotav	1413	70	4.1	2531	1	NTC1_MOUSE	Q61vd6 strongyloce
1341	70	4.1	486	2	Q84939	Q84939 porcine rot	1414	70	4.1	2829	2	Q61VD6	Q61vd6 strongyloce
1342	70	4.1	486	2	Q9QNA9	Q9qna9 human rotav	1415	70	4.1	4007	1	FRS1_HUMAN	Q86xx4 homo sapien
1343	70	4.1	507	2	Q9N3F2	Q9n3f2 caenorhabdi	1416	69.5	4.1	121	2	Q9FWN5	Q9fwN5 oryza sativ
1344	70	4.1	521	2	Q65257	Q65257 arabidopsis	1417	69.5	4.1	152	2	Q8Y6E4	Q8y6e4 listeria mo
1345	70	4.1	530	2	Q6F2D8	Q6f2d8 solanum dem	1418	69.5	4.1	152	2	Q71YS5	Q71ys5 listeria mo

1419	69.5	4.1	170	2	Q7WXA4	Q7wxa4 alcaligenes
1420	69.5	4.1	181	2	Q9APN6	Q9apn6 pseudalter
1421	69.5	4.1	186	2	Q7QMA2	Q7qma2 anopheles g
1422	69.5	4.1	191	1	WAP_MACEU	Q9n018 macropus eu
1423	69.5	4.1	209	2	Q64873	Q64873 arabidopsis
1424	69.5	4.1	232	2	Q6QRC5	Q6qrg5 eurycea spe
1425	69.5	4.1	232	2	Q6QRH5	Q6qrh5 eurycea tym
1426	69.5	4.1	232	2	Q6QRJ8	Q6qrl8 eurycea tym
1427	69.5	4.1	232	2	Q6QRJ5	Q6qrl5 eurycea tym
1428	69.5	4.1	232	2	Q6QRJ6	Q6qrl6 eurycea tym
1429	69.5	4.1	232	2	Q6QRJ7	Q6qrl7 eurycea tym
1430	69.5	4.1	232	2	Q6QRK1	Q6qrk1 eurycea tym
1431	69.5	4.1	232	2	Q6QRL0	Q6qrl0 eurycea tym
1432	69.5	4.1	232	2	Q6QRL1	Q6qrl1 eurycea tym
1433	69.5	4.1	232	2	Q6QRL3	Q6qrl3 eurycea tym
1434	69.5	4.1	232	2	Q6QRL3	Q6qrl3 eurycea tym
1435	69.5	4.1	250	2	Q9W0D2	Q9w0d2 drosophila
1436	69.5	4.1	253	2	Q9D8H2	Q9d8h2 m mus muscu
1437	69.5	4.1	257	2	Q8R202	Q8r202 mus musculu
1438	69.5	4.1	261	2	Q9D7L8	Q9d7l8 m mus muscu
1439	69.5	4.1	272	2	Q7Q5A5	Q7q5a5 anopheles g
1440	69.5	4.1	272	2	Q9XEN6	Q9xen6 tritlicum ae
1441	69.5	4.1	294	2	Q98QW9	Q98qw9 mycoplasma
1442	69.5	4.1	301	2	Q30621	Q30621 salmonella
1443	69.5	4.1	309	2	Q49746	Q49746 arabidopsis
1444	69.5	4.1	309	2	Q9SSR0	Q9ssr0 arabidopsis
1445	69.5	4.1	316	2	DF57_ARATH	Q9lsl6 arabidopsis
1446	69.5	4.1	326	2	Q87S03	Q87s03 vibrio para
1447	69.5	4.1	353	2	Q01562	Q01562 caenorhabdi
1448	69.5	4.1	356	2	Q19267	Q19267 caenorhabdi
1449	69.5	4.1	357	2	Q7P740	Q7p740 fusobacteri
1450	69.5	4.1	357	2	Q8BUP3	Q8bup3 mus musculu
1451	69.5	4.1	358	1	Y701_CHLPN	Q9z7k4 chlamydia p
1452	69.5	4.1	359	2	Q7VGZ8	Q7vgz8 helicobacte
1453	69.5	4.1	362	2	Q9LTC3	Q9ltc3 arabidopsis
1454	69.5	4.1	377	2	Q8BMT0	Q8bmt0 mus musculu
1455	69.5	4.1	380	2	Q35970	Q35970 thomabomys
1456	69.5	4.1	380	2	Q9XNW3	Q9xnw3 rhipidomys
1457	69.5	4.1	381	2	Q8M7D5	Q8m7d5 calomys cal
1458	69.5	4.1	399	2	Q8BGV2	Q8bgv2 mus musculu
1460	69.5	4.1	400	2	Q9D5T8	Q9d5t8 mus musculu
1461	69.5	4.1	409	2	Q7UHB8	Q7uhb8 rhodopirell
1462	69.5	4.1	419	2	Q21563	Q21563 caenorhabdi
1463	69.5	4.1	419	2	Q9NA38	Q9na38 caenorhabdi
1464	69.5	4.1	420	2	Q9NA61	Q9na61 caenorhabdi
1465	69.5	4.1	432	2	Q7N8Z4	Q7n8z4 photorhabdu
1466	69.5	4.1	452	2	Q8V5A8	Q8v5a8 caephallia e
1467	69.5	4.1	456	2	Q7RSB7	Q7rsb7 plasmodium
1468	69.5	4.1	456	2	Q8R0R0	Q8r0r0 mus musculu
1469	69.5	4.1	461	2	Q9B9U6	Q9b9u6 aulopus jap
1470	69.5	4.1	461	2	Q9EXY2	Q9exy2 escherichia
1471	69.5	4.1	472	2	Q95WM2	Q95wm2 papilio can
1472	69.5	4.1	473	2	Q8NKT4	Q8nkt4 acidianus a
1473	69.5	4.1	476	2	Q8XT06	Q8xt06 ralsstonia s
1474	69.5	4.1	484	2	Q7V4J9	Q7v4j9 prochloroco
1475	69.5	4.1	490	2	Q6IPW5	Q6ipw5 homo sapien
1476	69.5	4.1	500	2	Q8ZSS5	Q8zss5 salmonella
1477	69.5	4.1	502	2	Q95WX2	Q95wx2 papilio gla
1478	69.5	4.1	512	2	Q81915	Q81915 arabidopsis
1479	69.5	4.1	512	2	Q6PEZ8	Q6pez8 homo sapien
1480	69.5	4.1	513	2	Q8HV47	Q8hv47 kaempferia
1481	69.5	4.1	515	1	GMI1_METAC	Q8tm16 mehanosarc
1482	69.5	4.1	515	2	Q8HVI6	Q8hvi6 stahlianthu
1483	69.5	4.1	521	2	Q8XYV0	Q8xyv0 ralsstonia s
1484	69.5	4.1	537	2	Q6PWK7	Q6pwk7 pneumonia v
1485	69.5	4.1	560	2	Q8CET2	Q8cet2 mus musculu
1486	69.5	4.1	607	1	ELM3_MOUSE	Q8byz7 mus musculu
1487	69.5	4.1	608	2	Q9GMB0	Q9gmb0 eus scrofa
1488	69.5	4.1	615	2	Q69WY1	Q69wy1 cryza sativ
1489	69.5	4.1	626	2	Q65451	Q65451 arabidopsis
1490	69.5	4.1	651	2	Q6CNL5	Q6cnl5 kluyveromyc
1491	69.5	4.1	673	2	Q9DBR3	Q9dbtr3 mus musculu
			678	2	Q6ZWC1	Q6zwc1 homo sapien

1492	69.5	4.1	694	2	Q9FH01	Q9fh01 arabidopsis
1493	69.5	4.1	700	2	Q9FSB6	Q9fsb6 raphanus sa
1494	69.5	4.1	713	2	Q6GN18	Q6gn18 xenopus lae
1495	69.5	4.1	719	2	Q9U019	Q9u019 giardia lam
1496	69.5	4.1	719	2	Q9U021	Q9u021 giardia lam
1497	69.5	4.1	720	2	Q6PDE4	Q6pde4 mus musculu
1498	69.5	4.1	728	2	Q94439	Q94439 schizosacch
1499	69.5	4.1	743	2	Q8NPT3	Q8nft3 homo sapien
1500	69.5	4.1	743	2	Q7MAN9	Q7man9 wolfinella s

ALIGNMENTS

RESULT 1

CA08_HUMAN	STANDARD;	PRT;	323 AA.
AC	Q9BX54; 075393;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	25-JAN-2005 (Rel. 46, Last annotation update)		
DE	Protein Clorf8 precursor (liver membrane-bound protein) (HSPC001)		
DE	(UNQ169/PRO195).		
GN	Name=Clorf8;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Fetal liver;		
RA	Qu X., Zhang C., Zhai Y., Wu S., Yu Y., Wei H., Xing G., Lu C.,		
RA	Zhou G., Dong C., He F.;		
RT	"Homo sapiens liver membrane-bound protein mRNA.";		
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Umbilical cord blood;		
RX	MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;		
RA	Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,		
RA	Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,		
RA	Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;		
RT	"Cloning and functional analysis of cDNAs with open reading frames for		
RT	300 previously undefined genes expressed in CD34+ hematopoietic		
RT	stem/progenitor cells.";		
RL	Genome Res. 10:1546-1560(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,		
RA	Huang A., Kim H.-S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P., Gray A.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment.";		
RL	Genome Res. 13:2265-2270(2003).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the BSMAP family.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 6.

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CC
DR EMBL; AF290615; AAK28026.1; -.
DR EMBL; AF047439; AAC39890.1; ALT_INIT.
DR EMBL; AY359029; AAO89388.1; -.
DR EMBL; BC003106; AAH03106.1; ALT_INIT.
DR Genew; HGNC:1239; Clorf8.
DR H-InvdB; HIX000609; -.
DR Signal; Transmembrane.
KW SIGNAL 1 35 Potential.
FT CHAIN 36 323 Protein Clorf8.
FT DOMAIN 36 239 Extracellular (Potential).
FT TRANSMEM 240 262 Potential.
FT DOMAIN 263 323 Cytoplasmic (Potential).
FT CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 323 AA; 36223 MW; 0926AB7D12D1B902 CRC64;

Query Match 100.0%; Score 1694; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 7.2e-144;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPKGSIMVTRTQGLPPLLLITMALAGSGGTASAEAFDSVLGDTASCHRAQCQLTYPLHT 60
Db 1 MAAPKGSIMVTRTQGLPPLLLITMALAGSGGTASAEAFDSVLGDTASCHRAQCQLTYPLHT 60
QY 61 YPKBEELIYACQRCRLFSICQFVDDGIDLNRKLECSACTEAYSQSDEQYACHLGCONQ 120
Db 61 YPKBEELIYACQRCRLFSICQFVDDGIDLNRKLECSACTEAYSQSDEQYACHLGCONQ 120
QY 121 LPFAELRQEQLMSLMPKMHLLPPLTLVRSFWSMDMDSAQSFITSSWTFYLOADDGKIIVF 180
Db 121 LPFAELRQEQLMSLMPKMHLLPPLTLVRSFWSMDMDSAQSFITSSWTFYLOADDGKIIVF 180
QY 181 QSKPEIQAPHLEQEPFNLRSSLSKMSYLQMRNSQAHRNFLLEDGSDGFLRCLSLNSGW 240
Db 181 QSKPEIQAPHLEQEPFNLRSSLSKMSYLQMRNSQAHRNFLLEDGSDGFLRCLSLNSGW 240
QY 241 ILTTTLVLSVMVLWICCATVATAVEQYVPSEKLSIYGDLEFMNEOKLNRRYPASSLVVVR 300
Db 241 ILTTTLVLSVMVLWICCATVATAVEQYVPSEKLSIYGDLEFMNEOKLNRRYPASSLVVVR 300
QY 301 SKTEDHBEAGPLPTKVNLAHSEI 323
Db 301 SKTEDHBEAGPLPTKVNLAHSEI 323

RESULT 2
Q96KK7 PRELIMINARY; PRT; 324 AA.
ID Q96KK7

AC Q96KK7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Thymic dendritic cell-derived factor 1.
GN Name=Clorf8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016374; AAH16374.1; -.
SQ SEQUENCE 324 AA; 36262 MW; 59B10B582305275B CRC64;

Query Match 98.8%; Score 1674.5; DB 2; Length 324;
Best Local Similarity 99.4%; Pred. No. 4.1e-142;
Matches 322; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAPKGSIMVTRTQGLPPLLLITMALAGSGGTASAEAFDSVLGDTASCHRAQCQLTYPLHT 60
Db 1 MAAPKGSIMVTRTQGLPPLLLITMALAGSGGTASAEAFDSVLGDTASCHRAQCQLTYPLHT 60
QY 61 YPKBEELIYACQRCRLFSICQFVDDGIDLNRKLECSACTEAYSQSDEQYACHLGCONQ 120
Db 61 YPKBEELIYACQRCRLFSICQFVDDGIDLNRKLECSACTEAYSQSDEQYACHLGCONQ 120
QY 121 LPFAELRQEQLMSLMPKMHLLPPLTLVRSFWSMDMDSAQSFITSSWTFYLOADDGKIIVF 180
Db 121 LPFAELRQEQLMSLMPKMHLLPPLTLVRSFWSMDMDSAQSFITSSWTFYLOADDGKIIVF 180
QY 181 QSKPEIQAPHLEQEPFNLRSSLSKMSYLQMRNSQAHRNFLLEDGSDGFLRCLSLNSG 239
Db 181 QSKPEIQAPHLEQEPFNLRSSLSKMSYLQMRNSQAHRNFLLEDGSDGFLRCLSLNSG 240
QY 240 WILTTTLVLSVMVLWICCATVATAVEQYVPSEKLSIYGDLEFMNEOKLNRRYPASSLVVVR 299
Db 241 WILTTTLVLSVMVLWICCATVATAVEQYVPSEKLSIYGDLEFMNEOKLNRRYPASSLVVVR 300
QY 300 RSKTEDHBEAGPLPTKVNLAHSEI 323
Db 301 RSKTEDHBEAGPLPTKVNLAHSEI 324

RESULT 3
CA08_MOUSE

ID CA08 MOUSE STANDARD; PRT; 323 AA.
 AC Q9QY73; Q99LY8; Q9D1P9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein C1orf8 homolog precursor (Thymic dendritic cell-derived factor 1).
 OS Name=C1orf8; Synonyms=ORF18, Tdcf1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Thymus;
 RA Jin C.G., Chen W.F.;
 RT "Isolation and molecular cloning of gene encoding a novel dendritic
 RL cell-derived factor."
 RN Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo, and Liver;
 RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldeirali R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Bruce V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., Mckenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski B., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arawaka T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J, and FVB/N;
 RC TISSUE=Colon, Eye, Kidney, and Mammary gland;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
CC	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	- - SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC	- - SIMILARITY: Belongs to the BSMAP family.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF116911; AAF20283.1; -
DR	EMBL; AK003252; BAB22668.2; -
DR	EMBL; AK050162; BAC34103.1; -
DR	EMBL; BC002164; AAH02164.1; -
DR	EMBL; BC014732; AAH14732.1; -
DR	EMBL; BC018379; AAH18379.1; -
DR	EMBL; BC045145; AAH45145.1; -
DR	EMBL; BC058273; AAH58273.1; -
DR	MGI; MGI:1929278; ORF18.
KW	Signal; Transmembrane.
FT	SIGNAL 1 34 Potential.
FT	CHAIN 35 323 Protein Clorf8 homolog.
FT	TRANSMEM 240 262 Potential.
FT	CARBOHYD 90 90 N-linked (GlcNAc...) (Potential).
FT	CONFLICT 48 48 C -> V (in Ref. 1).
FT	CONFLICT 103 103 A -> T (in Ref. 1).
FT	CONFLICT 121 121 L -> W (in Ref. 1).
FT	CONFLICT 139 139 H -> Q (in Ref. 1).
FT	CONFLICT 221 222 YL -> DR (in Ref. 1).
FT	CONFLICT 248 248 L -> F (in Ref. 3; AAH45145).
FT	CONFLICT 264 264 A -> G (in Ref. 1).
FT	CONFLICT 277 300 YGDLEFMNEQKLSRYPAPLVIYR -> IGHFQFINQNLT TYPEPPLLIVK (in Ref. 1).
SEQUENCE	323 AA; 36313 MW; 0E9BF6B6E07C7D96 CRC64;
Query Match	95.1%; Score 1611; DB 1; Length 323;
Best Local Similarity	94.1%; Pred. No. 2.1e-136;
Matches 304; Conservative 11; Mismatches 8; Indels 0; Gaps 0	
QY :	1 MAAPKGSIMVTRTQLGLPPLLLITMALAGSGGTASABAFSDVLGDTASCHRACOLTYPLHT 60
Db	1 MAAPKGKLWQAQLGLPPLLLITMALAGSGGTAAAEAFDSVLGDTASCHRACOLTYPLHT 60
QY	61 YPKHEELYACQRCRLFSICQVDGIDLNRKLECESACTEAYSQSDEQYACHLGCOMQ 120
Db	61 YPKHEELYACQRCRLFSICQVDGDLNRTKLECESACTEAYSQPDEQYACHLGCOMQ 120
QY	121 LPFAELRQEQLMSLMPKMHLPLTLVRSFWSDMDMSAQSFTSSWTFFYLQADDGKIYIF 180
Db	121 LPFAELRQEQLMSLMPKMHLPLTLVRSFWSDMDMSAQSFTSSWTFFYLQADDGKIYIF 180
QY	181 QSKPEIQYAPHLEQEPFNURESSLKSMSYLOMRNSQAHRNFLEDGESDGFLRCLSLNSGW 240
Db	181 QSKPEIQYAPHLEQEPFNURESSLKSMSYLOMRNSQAHRNYIEESDGFRLRCLSLNSGW 240
QY	241 ILTTTLVLSVMWLWICCATAVAVEQYVPSEKLSIYGDLFEFNEQKLNRYPASSLVVR 300
Db	241 ILTTTLVLSVMWLWICCATAVAVEQYVPPEKLSIYGDLFEFNEQKLSRYPAPLSVIYR 300
QY	301 SKTEDHEEAGPLPTKVNLAHSEI 323
Db	301 SQTEEHBEAGPLPTKVNLAHSEI 323

DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Clorf8 protein (Fragment).
GN Name=Clorf8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062738; AAH62738.1; -.
FT NON TER 1 1
SQ SEQUENCE 239 AA; 27100 MW; F37D2FF1F83ED8F CRC64;

Query Match 72.8%; Score 1234; DB 2; Length 239;
Best Local Similarity 99.6%; Pred. No. 1.2e-102;
Matches 237; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 86 GIDLNRKLECESACTEAYSQSDEQYACHLGCONQLPFAELRQEOQLMSLMPKMLPPLT 145
Db 2 GIDLNRKLECESACTEAYSQSDEQYACHLGCONQLPFAELRQEOQLMSLMPKMLPPLT 61

QY 146 LVRSFWSMDMSAQSFTTSWTFYLLQADDGKIVIFQSKPEIQYAPHLQEPNTLRSSLS 205
Db 62 LVRSFWSMDMSAQSFTTSWTFYLLQADDGKIVILQSKPEIQYAPHLQEPNTLRSSLS 121

QY 206 KMSYLOMRNSQAHRNPLEDGEDSGFLRCLSLNSGWLTTTLVLSVMVLWICCATVATAY 265
Db 122 KMSYLOMRNSQAHRNPLEDGEDSGFLRCLSLNSGWLTTTLVLSVMVLWICCATVATAY 181

QY 266 EQYVPSEKLSIYGDLEFMNEOKLNRYPASSLVVVRSKTEDHEAGPLPTKYNLAHSEI 323
Db 182 EQYVPSEKLSIYGDLEFMNEOKLNRYPASSLVVVRSKTEDHEAGPLPTKYNLAHSEI 239

RESULT 5
Q6GNB1
ID Q6GNB1 PRELIMINARY; PRT; 324 AA.
AC Q6GNB1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MGC82908 protein.
GN Name=MGC82908;
OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodnae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073604; AAH73604.1; -.
SQ SEQUENCE 324 AA; 36080 MW; 786631B1D53DF8B0 CRC64;

Query Match 58.6%; Score 993.5; DB 2; Length 324;
Best Local Similarity 60.1%; Pred. No. 7.6e-81;
Matches 191; Conservative 39; Mismatches 75; Indels 13; Gaps 2;

QY 19 LLLTALAGSGGTASAEAFDSVLGDTASCHRAQQLTYPPLHTYPKBEELIYACQRCRLFS 78
Db 7 LVLVLLFCASARATEPAVNVDSVLEDSTSGHCVCDGTYPPLHTYPEEBELFACQRCRLFS 66

QY 79 ICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCONQLPFAELRQEOQLMSLMPKM 138
Db 67 ICQFVDDGIDLNRKLECESACTEAYVPQPTQYACNLGCHSQMPFAKROBELADLAPRI 126

QY 139 HLLFPLTLVRSFWSMDMSAQSFTS--SWTFYLLQADDGKIVIFQSKPEIQYAPHLQEP 196
Db 127 HLLFPLAFVGAFTWRDMLDSAQSFTGNPSWTFYVQADNGRIIVQSGSEIQLDPQFLSEK 186

QY 197 TNLRESSLSKMS-----YLQMRNSQAHRNPLEDGEDSGFLRCLSLNSGWLTTT 245
Db 187 TQPAESFLDKISLDLMPGPSTGQYGEERTWDQKSDSLNLDEGDNFLKCFSSANSNWLISVT 246

QY 246 LVLSVMVLWICCATVATAVEQYVPSEKLSIYGDLEFMNEOKLNRYPASSLVVVRSKTED 305
Db 247 LVLSVLVLLWICCATVATADQYIPSEKLSIYGDLEFMNEOKLHRYPATLVVHGPRPEE 306

QY 306 HEEAGPLPTKYNLAHSEI 323
Db 307 SEDAGPLPTKYDLTQSAI 324

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054584; AAH54584.1; -.
DR ZFIN; ZDB-GENE-040426-2651; zgc:63977.
SQ SEQUENCE 339 AA; 37263 MW; 1EE568E07627DEDA CRC64;

Query Match 35.2%; Score 595.5; DB 2; Length 339;
Best Local Similarity 39.5%; Pred. No. 5.2e-45;
Matches 134; Conservative 75; Mismatches 91; Indels 39; Gaps 11;

QY 15 GLPPLL-LITMALAGSGGTASAEAFDSVLGDTASCHRAQOLTYPLHTYPEKEELVACQRG 73
Db 10 GVPALVSLILVALA---AASSDLFDNQLGDINCYCKQCMSIKNKSPAKDSIMVACHRG 65

QY 74 CRLEFSICQFVDDGIDLNRITKECESACTEAYSQSDQYACHLGCONQLPFAELROEQLMS 133
Db 66 CRLYSICQFVNGNTGINTSKERCQACQEAYSKLEQACSTGCASQPAPEIKRRLKA 125

QY 134 LMPKMHLLPPLTVRSFWSMDMDSAQSFITSSWTFYLAQADGKIVIFQSKPEIQYA-PHL 192
Db 126 LTNRPKPISVMEAVSSWCNDIVSSAQSFISSTWTFYLAQADGKVVVFQSQPEIEYSLPEL 185

QY 193 EGEPTNL-----RESSLSKMSYLOMRNSQAHNFLDEGSD-G 229
Db 186 QAPRSNVVDKWPQVNSHTQRPHTGGRHLHRERNAKPG-VKGNVSOH--AEDPAAEHD 241

QY 230 FLRCLSLNSG---WILTTVLVSVVWLWICCATVATAVEQYVPSEKLSITYGLEPANE- 285
Db 242 FLGCMSSRRSGLPRWILAACFLISIMVWLMLSCASLVTAPEQHIKTQ-LSINGDKPEYDDA 300

QY 286 QKLNRYPASSLNVVR-SKTEPDHEAGPLPTKVNLAHSEI 323
Db 301 QKVNPHYLTPIAMTIAQSESKAAGPLPVKVDLSKTSI 339

RESULT 9
BMAP_HUMAN
ID BMAP_HUMAN STANDARD; PRT; 342 AA.
AC Q9UK28;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Brain specific membrane-anchored protein precursor.
GN Name=BSMAP; Synonyms=C19orf4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99458621; PubMed=10527841; DOI=10.1006/birc.1999.1481;
RA Elson G.C.A., Benoit de Coignac A., Aubry J.-P., Delneste Y.,
RA Magistrelli G., Holzwarth J., Bonnefoy J.-Y., Gauchat J.-F.;
RT "BSMAP, a novel protein expressed specifically in the brain whose gene
RT is localized on chromosome 19p12.";
RL Biochem. Biophys. Res. Commun. 264:55-62(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May have a role in brain function.
CC -1- SUBCELLULAR LOCATION: Could be associated with an intracellular
CC : organelle or membrane (Potential).
CC -1- TISSUE SPECIFICITY: Expressed preferentially at high level in the
CC : brain.
CC -1- SIMILARITY: Belongs to the BSMAP family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AF186264; AAF00529.1; -.
DR EMBL; BC010446; AAH10446.1; -.
DR PIR; JC7110; JC7110.
DR Genew; HGNC:13237; C19orf4.
DR H-InvDB; HIX0014920; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
KW Signal; Transmembrane.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 342 Brain specific membrane-anchored protein.
FT TRANSMEM 268 290 Potential.
FT SITE 340 342 Microbody targeting signal (Potential).
FT CARBOHYD 97 97 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 342 AA; 37619 MW; FB56B6B37AF62569 CRC64;

Query Match 25.0%; Score 423.5; DB 1; Length 342;
Best Local Similarity 33.5%; Pred. No. 1.6e-29;
Matches 107; Conservative 56; Mismatches 115; Indels 41; Gaps 8;

QY 16 LPPLLITMALA---GSGGTASAEAFDSVLGDTASCHRAQOLTYPLHTYPEKEEL----- 67
Db 7 MPPPLLITLLASPPPAASAPARDPFAPQLGDTQNCQLRCR-DRDLGPQPSAGLEGASE 65

QY 68 -----YACQRCRLFSICQFVDDGIDLNRITKECESACTEAYSQSDQYACHLGCG 118
Db 66 SPYDRAVLISACERGRLFSICRFVARSSKPNATQTECEACVEAYVKEAQQACSHGCW 125

QY 119 NQLPFAELROEQLMSLMPKMHLLPPLTVRSFWSMDMDSAQSFITSSWTFYLAQADGKIV 178
Db 126 SQPAPEPEQKRYLEAPSGALSL-LDLFSTLCNDLVNSAQGFVSSWTYYLQTDNGKV 184

QY 179 IFQSKPEIQ---YAPHLEQEPNLRSE-----SLSKM--SYLOMRNSQAH 219
Db 185 VFQTPIVESLGRQGGRLQRVETWRGSHPEALVHVDVPGPLDKYKAKIRVKTSSKAK 244

QY 220 NFLEGESDGLRCLSLNSG---WILTTVLVSVVWLWICCATVATAVEQYVPSEKLSI 276
Db 245 VESEEPQDNDFLSCMSRRSGLPRWILAACFLSVLWMLWSCSTLVTAPEGHLKFQPLTL 304

QY 277 YGDLFEMNEQKLNRYPASS 295
Db 305 EQHKGFMPEPDPPLYPSPS 323

RESULT 10

07TN12
ID 07TN12 PRELIMINARY; PRT; 337 AA.
AC 07TN12;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE RIKEN cDNA 5330410G16.
GN Name=5330410G16R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056172; AAH56172.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
SQ SEQUENCE 337 AA; 37661 MW; F58B93B072453E3A CRC64;

Query Match 24.5%; Score 415.5; DB 2; Length 337;
Best Local Similarity 34.3%; Pred. No. 8.1e-29;
Matches 107; Conservative 52; Mismatches 112; Indels 41; Gaps 9;

QY 18 PLLLLTALAGSGSTASAEAFDSVLGDTASCHRAQCLTYPLHTYPKEE----- 66
DB 7 PLLLLLASLV--TTPPADPFAFPQLGDTORCQQRCKQHNP-GSPPAQPEPEGPSSEPNK 63
QY 67 ---LYACORGCRLFSICQFVDDGIDLNRTKLECEBSACTEAYSQSDEQYACHLGCONQLPF 123
DB 64 AILISACERGLFSICRFVAKSSRPNATETECBACTEAYVKAERACSEGCWQIPE 123
QY 124 AELRQQL-MSLMPKMLLPPLTLVRSFWSMDMDSAQSFITSSWTFYLAADGKIYFQS 182
DB 124 PETOLEQKDLDPRGRSLRYLFSMLCSDLMSSAQGFSSWYSLQTDNRKVVVFQT 183
QY 183 KPEIQ----YAPHLEQPTNLRSE-----SLSKM--SYLQMRNSQAHNPLE 223
DB 184 QPVAENFAFGSHLQREVEVTRRSHPKALELHMDPVGPLDKVRKAKPRVTKSKAYESED 243
QY 224 DGESDGLRCLSLNSG---WILTTTLVLSVMVLWICATVATAVEQYVPSEKLSIYIDL 280
DB 244 QQESD-FLSCMSRSGLPRLVFLCCLFLSLILMLWLSGCTLVTTPGQHLKFPPLTAQHK 302
QY 281 EFMNEQKLNRYP 292
DB 303 GLLVESDWP LYP 314

RESULT 11
ID 081YZ6 PRELIMINARY; PRT; 832 AA.
AC 081YZ6;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein MGCC33370.
GN Name=MGCC33370;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032859; AAH32859.1; -.
KW Hypothetical protein.
SQ SEQUENCE 832 AA; 95559 MW; 54BDC52DCC4F0C03 CRC64;

Query Match 6.1%; Score 104; DB 2; Length 832;
Best Local Similarity 25.5%; Pred. No. 2.8;
Matches 50; Conservative 31; Mismatches 71; Indels 44; Gaps 10;

QY 137 KMHLLPPLTLVRSFWSMDMDSAQSFITSSWTFYLAQ-ADGKIYVIFQSKPEIQ-YAPHLE 193
DB 529 KLHL-----WTNVTTRAFFILSTSGQTFYLAADDGTI-----QIDYPLHL 571
QY 194 QEPNLRSSLSKMSYLQMRNSQAH-RNFLLEDG-----ESDGLRCLSLNSGW 240
DB 572 AQ--SIAFTTKDKCPYMAFHNNAHVFFLDKGEALTWQTQIVYPENTGLYVIVESYGP 629
QY 241 ILTTTLVLSVMVLWICATVATAVEQYVPSEKLSIYDLEFMNEQKLNRYPPASSLVVR 300
DB 630 ILQESHEISFEAFGYCTKTLTLTFYQNVYERISDY----FETQDK-----HTGLVLVQ 680
QY 301 SKTEDHEAGPLPTKV 316
DB 681 FRPSEYSKACP IAKV 696

RESULT 12
ID 081713 PRELIMINARY; PRT; 1250 AA.
AC 081713;
DT 01-MAR-2003 (TReMBLrel. 23, Created)

01-MAR-2003 (Tremblrel. 23, last sequence update)
01-JUN-2003 (Tremblrel. 24, last annotation update)
Roller: helically twisted, animals roll when moving protein 3, isoform b.
GN Name=rol-3; ORFNames=C16D9.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Gattung S., Le T.T.;
RA "The sequence of C. elegans cosmid C16D9."; Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL [4]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Wilson R.; Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL [5]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64858; AAN84865.1; -.
DR WormBase; WBGene00004395; rol-3.
DR WormPep; C16D9.2b; CE32799.
SQ SEQUENCE 1250 AA; 139843 MW; 268723A717DA6A05 CRC64;
Query Match 6.0%; Score 102; DB 2; Length 1250;
Best Local Similarity 21.7%; Pred. No. 7;
Matches 65; Conservative 38; Mismatches 97; Indels 100; Gaps 16;
QY 34 SAEAFDSVLGDTASCHRAQ---LTYPLHT-----YPKEELYACQRCRLFSIC 80
DB 25 SATVFSSSL--KTCQSQCEERNLAYPLDSGEVHWTGLAEVNYSSRISSCRHGCE----- 76
QY 81 QFVDDGIDLNRTKLECESACTEAVSQSDEQYACHLGCONQL-PAELRQEQLMSPKMH 139
DB 77 -----DVDERESKCDVKCSEEGIVSN---ACKQGCRAVLVSFLAQAOALLIQVHVNME 126
QY 140 LL-----FPLTLVRS-----FWSMDMDSAQSFTSSWTFYLLQADDGKIVIFQ 181
DB 127 VLETSMKLKWEPETLAEELKEIANADIFWFSQTKPLNGILGWRWT----- 172
QY 182 SKPEIQYAPHLQEPTNLRESSLSKM-----SYLQMRNSQAHNPLFLEDGESDGLRC 233
DB 173 SLFQ-----NSFRNSSLSSEVHVPEFGEHVEVRLALSYRNQVLVSRTTYHLR 221
QY 234 LSLNSGWLTTTLVLSVMVL---LWICATVATAVEQYVPSEKLSIYGDLEFMNEQKLN 289
DB 222 LS-KSG---TLLEVIQQLQLSDDRVAVCYRT-----NQPTPKFKLITM-----TLNDNTIN 268
RESULT 13
Q81715 PRELIMINARY; PRT; 2456 AA.
AC Q81715;
DT 01-MAR-2003 (Tremblrel. 23, Created)

01-MAR-2003 (Tremblrel. 23, last sequence update)
01-MAR-2004 (Tremblrel. 26, last annotation update)
Roller: helically twisted, animals roll when moving protein 3, isoform a.
GN Name=rol-3; ORFNames=C16D9.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Gattung S., Le T.T.;
RA "The sequence of C. elegans cosmid C16D9."; Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL [4]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RA Wilson R.; Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL [5]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64858; AAN84864.1; -.
DR HSSP; P08581; 1RLW.
DR WormBase; WBGene00004395; rol-3.
DR WormPep; C16D9.2a; CE32798.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00041; fn3; 3.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50853; FN3; 2.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
SQ SEQUENCE 2456 AA; 273833 MW; BBFABBC75FF82B8 CRC64;
Query Match 6.0%; Score 102; DB 2; Length 2456;
Best Local Similarity 21.7%; Pred. No. 17;
Matches 65; Conservative 38; Mismatches 97; Indels 100; Gaps 16;
QY 34 SAEAFDSVLGDTASCHRAQ---LTYPLHT-----YPKEELYACQRCRLFSIC 80
DB 25 SATVFSSSL--KTCQSQCEERNLAYPLDSGEVHWTGLAEVNYSSRISSCRHGCE----- 76
QY 81 QFVDDGIDLNRTKLECESACTEAVSQSDEQYACHLGCONQL-PAELRQEQLMSPKMH 139
DB 77 -----DVDERESKCDVKCSEEGIVSN---ACKQGCRAVLVSFLAQAOALLIQVHVNME 126
QY 140 LL-----FPLTLVRS-----FWSMDMDSAQSFTSSWTFYLLQADDGKIVIFQ 181
DB 127 VLETSMKLKWEPETLAEELKEIANADIFWFSQTKPLNGILGWRWT----- 172

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OM protein - protein search, using sw model

Run on: March 28, 2005, 13:08:45 ; Search time 24 Seconds
(without alignments)
1004.652 Million cell updates/sec

Title: US-09-978-299A-330
Perfect score: 1694
Sequence: 1 MAAPKGSIMVTRQGLPPL.....EDHEAGPLPTKVNLAHSEI 323

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1694	100.0	323	4	US-09-976-594-818 Sequence 818, App
2	1262.5	74.5	273	4	US-09-149-476-476 Sequence 476, App
3	707	41.7	132	4	US-09-513-999C-4172 Sequence 4172, Ap
4	96	5.7	963	4	US-09-949-016-11519 Sequence 11519, A
5	96	5.7	963	4	US-09-949-016-11520 Sequence 11520, A
6	95.5	5.6	915	4	US-09-907-794A-34 Sequence 34, Appl
7	95.5	5.6	915	4	US-09-905-125A-34 Sequence 34, Appl
8	95.5	5.6	915	4	US-09-902-775A-34 Sequence 34, Appl
9	95.5	5.6	915	4	US-09-906-700-34 Sequence 34, Appl
10	95.5	5.6	915	4	US-09-903-603A-34 Sequence 34, Appl
11	95.5	5.6	915	4	US-09-904-920A-34 Sequence 34, Appl
12	95.5	5.6	915	4	US-09-909-064-34 Sequence 34, Appl
13	95.5	5.6	915	4	US-09-905-381A-34 Sequence 34, Appl
14	95.5	5.6	915	4	US-09-906-618-34 Sequence 34, Appl
15	93.5	5.5	956	4	US-09-949-016-6215 Sequence 6215, Ap
16	86	5.1	1106	4	US-09-949-016-9626 Sequence 9626, Ap
17	85.5	5.0	2733	4	US-09-949-016-11433 Sequence 11433, A
18	85.5	5.0	3259	4	US-09-949-016-6507 Sequence 6507, Ap
19	84	5.0	1350	2	US-08-319-866-9 Sequence 9, Appli
20	84	5.0	1350	4	US-08-809-917-9 Sequence 9, Appli
21	83	4.9	503	4	US-09-198-452A-263 Sequence 263, App
22	83	4.9	508	4	US-09-438-185A-253 Sequence 253, App
23	82.5	4.9	698	4	US-09-107-532A-5685 Sequence 5685, Ap
24	82	4.8	119	3	US-09-046-479-4 Sequence 4, Appli
25	82	4.8	119	3	US-08-822-897C-4 Sequence 4, Appli
26	82	4.8	119	4	US-09-608-810A-5 Sequence 5, Appli
27	82	4.8	119	4	US-09-404-417A-4 Sequence 4, Appli

28	82	4.8	119	4	US-09-794-987-4 Sequence 4, Appli
29	82	4.8	1564	4	US-09-976-594-309 Sequence 309, App
30	82	4.8	1609	4	US-09-562-702A-22 Sequence 22, Appl
31	82	4.8	1609	4	US-09-561-818A-22 Sequence 22, Appl
32	82	4.8	1617	4	US-09-562-702A-26 Sequence 26, Appl
33	82	4.8	2158	4	US-10-144-198-34 Sequence 34, Appl
34	82	4.8	2265	4	US-10-144-198-35 Sequence 35, Appl
35	82	4.8	2697	4	US-10-144-198-12 Sequence 12, Appl
36	81.5	4.8	566	1	US-07-955-905A-2 Sequence 2, Appli
37	81.5	4.8	566	1	US-07-955-905A-22 Sequence 22, Appl
38	81.5	4.8	1312	2	US-08-687-080-51 Sequence 51, Appl
39	81	4.8	485	3	US-08-378-313-27 Sequence 27, Appl
40	81	4.8	485	3	US-08-378-313-32 Sequence 32, Appl
41:	81	4.8	959	4	US-09-107-433-4334 Sequence 4334, Ap
42	81	4.8	1032	4	US-09-583-110-3366 Sequence 3366, Ap
43	81	4.8	1609	4	US-09-538-092-900 Sequence 900, App
44	80.5	4.8	453	3	US-09-171-461-48 Sequence 48, Appl
45	80.5	4.8	453	4	US-09-328-352-6445 Sequence 6445, Ap
46	80	4.7	305	4	US-09-970-711-48 Sequence 30, Appl
47	80	4.7	1605	4	US-09-562-702A-30 Sequence 26, Appl
48	80	4.7	1605	4	US-09-561-818A-26 Sequence 25, Appl
49	79.5	4.7	485	3	US-08-378-313-25 Sequence 710, App
50	79.5	4.7	703	3	US-09-710-279-710 Sequence 3015, Ap
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52	79.5	4.7	999	4	US-09-747-371-2 Sequence 1, Appli
53	79	4.7	638	2	US-08-897-443-1 Sequence 2, Appli
54	79	4.7	1118	1	US-07-934-393B-2 Sequence 2, Appli
55	79	4.7	1118	1	US-08-278-089A-2 Sequence 2, Appli
56	79	4.7	1118	2	US-08-838-957A-2 Sequence 2, Appli
57	79	4.7	1122	1	US-08-278-089A-6 Sequence 6, Appli
58	79	4.7	1122	2	US-08-838-957A-6 Sequence 16175, A
59	78.5	4.6	785	4	US-09-902-540-16175 Sequence 148, App
60	78.5	4.6	1312	2	US-08-592-126-148 Sequence 148, App
61	78.5	4.6	1312	4	US-09-168-595-148 Sequence 175, App
62	78	4.6	880	4	US-09-556-877-175 Sequence 175, App
63	78	4.6	880	4	US-09-620-412C-175 Sequence 175, App
64	78	4.6	880	4	US-09-598-419-175 Sequence 7884, Ap
65	77.5	4.6	447	4	US-09-949-016-7884 Sequence 16, Appl
66	77.5	4.6	462	1	US-08-417-330A-16 Sequence 29, Appl
67	77.5	4.6	530	1	US-08-307-499-29 Sequence 29, Appl
68	77.5	4.6	530	1	US-09-299-268-29 Sequence 27, Appl
69	77.5	4.6	669	4	US-09-345-473E-27 Sequence 5481, Ap
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71	77	4.5	1101	2	US-08-469-537A-96 Sequence 10242, A
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73	76.5	4.5	657	3	US-08-508-761B-2 Sequence 3, Appli
74	76.5	4.5	956	2	US-08-897-443-3 Sequence 8, Appli
75	76	4.5	357	4	US-09-535-909-8 Sequence 4300, Ap
76	76	4.5	462	3	US-09-134-001C-4300 Sequence 598, App
77	76	4.5	464	4	US-09-538-092-598 Sequence 16430, A
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79	76	4.5	487	4	US-09-535-909-4 Sequence 45293, A
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81	76	4.5	770	4	US-09-784-316-5 Sequence 2, Appli
82	76	4.5	770	4	US-08-426-627-2 Sequence 5, Appli
83	76	4.5	811	1	US-08-426-627-22 Sequence 22, Appl
84	76	4.5	811	1	US-08-426-627-22 Sequence 9215, Ap
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86	75.5	4.5	323	4	US-09-516-065-30 Sequence 30, Appl
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91	75	4.4	402	3	US-08-709-974A-4 Sequence 4, Appli
92	75	4.4	415	3	US-09-069-632-1 Sequence 27, Appl
93	75	4.4	415	3	US-08-361-920-27 Sequence 27, Appl
94	75	4.4	435	1	US-08-479-939-27 Sequence 27, Appl
95	75	4.4	435	1	US-08-483-432-27 Sequence 3, Appli
96	75	4.4	435	3	US-09-069-632-3 Sequence 189, App
97	75	4.4	435	3	US-09-556-877-189 Sequence 189, App
98	75	4.4	866	4	US-09-620-412C-189 Sequence 189, App
99	75	4.4	866	4	US-09-598-419-189 Sequence 189, App
100	75	4.4	866	4	US-09-598-419-189 Sequence 189, App

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104	74.5	4.4	546	US-09-949-016-8514	Sequence 8514, Ap
105	74.5	4.4	627	US-09-949-016-9447	Sequence 9447, Ap
106	74.5	4.4	761	US-09-949-016-6880	Sequence 6880, Ap
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115	74.5	4.4	1439	US-09-902-540-14072	Sequence 14072, A
116	74.5	4.4	2482	US-08-328-254-6	Sequence 6, Appli
117	74.5	4.4	3210	US-09-538-092-1154	Sequence 1154, Ap
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119	74.5	4.4	3248	PCT-US95-16216-1	Sequence 1, Appli
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124	74	4.4	628	US-09-903-012B-20	Sequence 20, Appl
125	74	4.4	628	US-09-900-797-20	Sequence 20, Appl
126	74	4.4	629	US-09-360-237-60	Sequence 60, Appl
127	74	4.4	1049	US-09-522-666-6	Sequence 6, Appli
128	74	4.4	1141	US-08-131-365B-54	Sequence 54, Appl
129	74	4.4	1141	US-08-668-123-54	Sequence 54, Appl
130	74	4.4	3924	US-09-538-092-1246	Sequence 1246, Ap
131	73.5	4.3	304	US-09-248-796A-20714	Sequence 20714, A
132	73.5	4.3	351	US-09-270-767-43939	Sequence 43939, A
133	73	4.3	589	US-09-543-681A-7643	Sequence 7643, Ap
134	73	4.3	679	US-09-252-991A-18681	Sequence 18681, A
135	72.5	4.3	946	PCT-US95-08493-13	Sequence 13, Appl
136	72.5	4.3	1213	US-09-543-681A-6478	Sequence 6478, Ap
137	72.5	4.3	1451	US-08-308-872B-4	Sequence 4, Appli
138	72	4.3	299	US-09-248-796A-15007	Sequence 15007, A
139	72	4.3	315	US-09-134-001C-3561	Sequence 3561, Ap
140	72	4.3	336	US-09-949-016-8140	Sequence 8140, Ap
141	72	4.3	415	US-08-833-642A-5	Sequence 5, Appli
142	72	4.3	430	US-09-198-452A-1038	Sequence 1038, Ap
143	72	4.3	436	US-09-438-185A-968	Sequence 968, App
144	72	4.3	1183	US-09-107-532A-6680	Sequence 6680, Ap
145	72	4.3	2753	US-09-949-016-7659	Sequence 7659, Ap
146	72	4.3	2753	US-09-949-016-7660	Sequence 7660, Ap
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148	71.5	4.2	1247	US-09-404-627-2	Sequence 2, Appli
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153	71	4.2	386	US-09-949-016-10000	Sequence 10000, A
154	71	4.2	429	US-08-339-152A-33	Sequence 33, Appl
155	71	4.2	438	US-09-380-682-58	Sequence 58, Appl
156	71	4.2	669	US-09-949-016-6720	Sequence 6720, Ap
157	71	4.2	836	US-08-426-627-6	Sequence 6, Appli
158	71	4.2	1021	US-09-252-991A-19205	Sequence 19205, A
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160	70.5	4.2	453	US-09-198-452A-875	Sequence 875, App
161	70.5	4.2	501	US-09-438-185A-818	Sequence 818, App
162	70.5	4.2	525	US-09-949-016-6353	Sequence 6353, Ap
163	70.5	4.2	575	US-09-134-000C-4457	Sequence 4457, Ap
164	70.5	4.2	605	US-08-190-802A-49	Sequence 49, Appl
165	70.5	4.2	605	US-08-477-346-49	Sequence 49, Appl
166	70.5	4.2	605	US-08-473-089-49	Sequence 49, Appl
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172	70.5	4.2	680	US-08-761-136-1	Sequence 1, Appli
173	70.5	4.2	680	US-09-576-967-1	Sequence 1, Appli
174	70.5	4.2	680	US-10-219-541-1	Sequence 1, Appli
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180	70.5	4.2	2842	US-08-289-548A-7	Sequence 7, Appli
181	70.5	4.2	2842	US-08-452-654-7	Sequence 7, Appli
182	70.5	4.2	2842	US-08-449-731-7	Sequence 2, Appli
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193	70.5	4.2	2843	US-09-538-092-1007	Sequence 1007, Ap
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195	70.5	4.2	2973	US-09-003-687A-7	Sequence 7, Appli
196	70.5	4.2	2973	US-09-136-605-7	Sequence 5, Appli
197	70	4.1	200	US-08-709-979A-5	Sequence 8, Appli
198	70	4.1	200	US-08-709-974A-8	Sequence 959, App
199	70	4.1	264	US-10-101-464A-959	Sequence 396, App
200	70	4.1	269	US-09-538-092-396	Sequence 272, App
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204	69.5	4.1	256	US-09-371-056-8	Sequence 2, Appli
205	69.5	4.1	310	US-09-371-056-2	Sequence 8488, Ap
206	69.5	4.1	344	US-09-489-039A-8488	Sequence 743, App
207	69.5	4.1	358	US-09-198-452A-743	Sequence 703, App
208	69.5	4.1	363	US-09-438-185A-703	Sequence 8224, Ap
209	69.5	4.1	469	US-09-489-039A-8224	Sequence 14489, A
210	69.5	4.1	604	US-09-248-796A-14489	Sequence 4, Appli
211	69.5	4.1	777	US-08-477-396A-4	Sequence 6, Appli
212	69.5	4.1	1198	US-09-949-016-6989	Sequence 6989, Ap
213	69.5	4.1	1199	US-10-023-894-2	Sequence 2, Appli
214	69.5	4.1	1203	US-09-949-016-10916	Sequence 10916, A
215	69	4.1	196	US-09-371-056-6	Sequence 6, Appli
216	69	4.1	256	US-09-148-545-180	Sequence 180, App
217	69	4.1	256	US-09-949-016-10522	Sequence 10522, A
218	69	4.1	375	US-09-328-352-6078	Sequence 6078, Ap
219	69	4.1	397	US-08-506-296B-59	Sequence 59, Appl
220	69	4.1	515	US-09-134-000C-4651	Sequence 4651, Ap
221	69	4.1	545	US-09-949-016-6469	Sequence 6469, Ap
222	69	4.1	558	US-09-949-016-7736	Sequence 7736, Ap
223	69	4.1	589	US-09-438-185A-459	Sequence 459, App
224	69	4.1	635	US-08-506-296B-71	Sequence 71, Appl
225	69	4.1	636	US-09-198-452A-489	Sequence 489, App
226	69	4.1	637	US-09-360-545-6	Sequence 6, Appli
227	69	4.1	637	US-09-398-395A-58	Sequence 58, Appl
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229	69	4.1	637	US-09-895-752-58	Sequence 58, Appl
230	69	4.1	637	US-09-903-012B-58	Sequence 58, Appl
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233	69	4.1	704	US-09-733-764-2	Sequence 12499, A
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235	69	4.1	977	US-09-590-656-1	Sequence 1, Appli
236	69	4.1	977	US-09-733-764-1	Sequence 45831, A
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239	69	4.1	1124	US-09-949-016-5946	Sequence 2, Appli
240	69	4.1	1124	PCT-US93-06093-2	Sequence 2, Appli
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243	69	4.1	1260	US-09-170-496D-292	Sequence 292, App
244	69	4.1	1293	US-09-364-425B-57	Sequence 57, Appl
245	69	4.1	1822	US-09-949-016-7999	Sequence 7999, Ap
246	69	4.1	2037	US-09-543-681A-5538	Sequence 5538, Ap

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249	68.5	4.0	258	4	US-09-270-767-43689	Sequence 43689, A
250	68.5	4.0	290	4	US-09-328-352-6785	Sequence 6785, Ap
251	68.5	4.0	299	4	US-09-248-796A-22243	Sequence 22243, A
252	68.5	4.0	327	4	US-09-248-796A-14761	Sequence 14761, A
253	68.5	4.0	339	4	US-09-270-767-41384	Sequence 41384, A
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258	68.5	4.0	737	1	US-08-185-432-4	Sequence 4, Appli
259	68.5	4.0	737	4	US-09-866-028-15	Sequence 15, Appl
260	68.5	4.0	737	4	US-09-944-457-15	Sequence 15, Appl
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262	68.5	4.0	1022	4	US-09-949-016-9041	Sequence 9041, Ap
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264	68.5	4.0	1102	4	US-09-358-383C-36	Sequence 36, Appli
265	68.5	4.0	1170	4	US-09-462-136-6	Sequence 6, Appli
266	68.5	4.0	1454	3	US-08-392-459-22	Sequence 22, Appl
267	68.5	4.0	1454	4	US-09-854-799-22	Sequence 22, Appl
268	68.5	4.0	1454	5	PCT-US91-08525-22	Sequence 22, Appl
269	68.5	4.0	1454	5	PCT-US93-04384-2	Sequence 2, Appli
270	68.5	4.0	1454	5	PCT-US93-04384-43	Sequence 43, Appl
271	68.5	4.0	1454	5	PCT-US93-04384-45	Sequence 45, Appl
272	68.5	4.0	1454	5	PCT-US93-04384-48	Sequence 48, Appl
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274	68	4.0	167	4	US-09-711-164-465	Sequence 465, App
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276	68	4.0	174	4	US-09-489-039A-9228	Sequence 9228, Ap
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279	68	4.0	174	4	US-09-489-039A-11342	Sequence 11342, A
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281	68	4.0	174	4	US-09-489-039A-11926	Sequence 11926, A
282	68	4.0	174	4	US-09-489-039A-12078	Sequence 12078, A
283	68	4.0	174	4	US-09-489-039A-12619	Sequence 12619, A
284	68	4.0	185	4	US-09-562-737-112	Sequence 112, App
285	68	4.0	287	4	US-09-949-016-11191	Sequence 11191, A
286	68	4.0	299	3	US-09-134-001C-4167	Sequence 4167, Ap
287	68	4.0	334	4	US-09-543-681A-6301	Sequence 6301, Ap
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289	68	4.0	337	4	US-09-516-065-32	Sequence 32, Appl
290	68	4.0	370	4	US-09-270-767-45912	Sequence 45912, A
291	68	4.0	375	4	US-09-311-021-8	Sequence 8, Appli
292	68	4.0	452	4	US-08-809-802-12	Sequence 12, Appl
293	68	4.0	456	4	US-09-482-273-227	Sequence 227, App
294	68	4.0	456	4	US-09-328-352-4415	Sequence 4415, Ap
295	68	4.0	457	4	US-09-482-273-189	Sequence 189, App
296	68	4.0	612	2	US-08-933-750C-36	Sequence 36, Appl
297	68	4.0	612	3	US-09-234-613-36	Sequence 36, Appl
298	68	4.0	613	4	US-09-328-352-6932	Sequence 6932, Ap
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304	68	4.0	807	4	US-09-280-597-1	Sequence 1, Appli
305	68	4.0	807	4	US-09-949-016-7356	Sequence 7356, Ap
306	68	4.0	1005	4	US-09-949-016-6968	Sequence 6968, Ap
307	68	4.0	1005	4	US-09-949-016-10620	Sequence 10620, A
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311	67.5	4.0	216	4	US-09-620-412C-20	Sequence 20, Appl
312	67.5	4.0	216	4	US-09-410-568-20	Sequence 20, Appl
313	67.5	4.0	216	4	US-09-598-419-20	Sequence 20, Appl
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317	67.5	4.0	565	4	US-09-134-000C-5782	Sequence 5782, Ap
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321	67.5	4.0	639	3	US-09-376-856-2	Sequence 2, Appli
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323	67.5	4.0	647	4	US-09-389-956-6	Sequence 6, Appli
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331	67.5	4.0	1180	5	PCT-US94-07902-28	Sequence 28, Appl
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333	67.5	4.0	1380	4	US-09-949-016-11688	Sequence 11688, A
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335	67.5	4.0	1895	2	US-08-619-554-4	Sequence 4, Appli
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337	67.5	4.0	2227	4	US-09-653-499-4	Sequence 4, Appli
338	67.5	4.0	2227	4	US-10-135-988-4	Sequence 4, Appli
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341	67	4.0	283	4	US-09-438-185A-462	Sequence 462, App
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343	67	4.0	313	4	US-09-148-545-233	Sequence 233, App
344	67	4.0	404	4	US-09-248-796A-18878	Sequence 18878, A
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346	67	4.0	439	4	US-09-248-796A-15955	Sequence 15955, A
347	67	4.0	455	4	US-09-710-279-2648	Sequence 2648, Ap
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351	67	4.0	557	1	US-08-608-267-4	Sequence 4, Appli
352	67	4.0	557	1	US-08-608-452-4	Sequence 4, Appli
353	67	4.0	557	1	US-08-608-224-4	Sequence 4, Appli
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375	66.5	3.9	303	4	US-09-710-279-1140	Sequence 1140, Ap
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377	66.5	3.9	329	2	US-08-742-605D-4	Sequence 4, Appli
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410	66	3.9	295	4	US-10-270-878-51	Sequence 898, App
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438	66	3.9	1436	4	US-09-578-063-78	Sequence 78, Appl
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463	65.5	3.9	448	4	US-09-198-452A-216	Sequence 216, App
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545	65	3.8	1002	4	US-09-604-287A-475	Sequence 475, App
546	65	3.8	1002	4	US-09-834-759-475	Sequence 475, App
547	65	3.8	1002	4	US-09-590-751A-475	Sequence 475, App
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571	64.5	3.8	214	1	US-07-739-142-12	Sequence 24, Appl
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586	64.5	3.8	386	4	US-09-739-861A-5	Sequence 5, Appli
587	64.5	3.8	386	4	US-09-795-583-5	Sequence 6022, Ap
588	64.5	3.8	386	4	US-09-949-016-6022	Sequence 235, App
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631	64	3.8	466	4	US-09-433-826B-472	Sequence 472, App
632	64	3.8	466	4	US-09-604-287A-472	Sequence 472, App
633	64	3.8	466	4	US-09-834-759-472	Sequence 472, App
634	64	3.8	466	4	US-09-590-751A-472	Sequence 472, App
635	64	3.8	466	4	US-09-551-621-472	Sequence 472, App
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658	64	3.8	1276	3	US-08-446-648-24	Sequence 24, Appl
659	64	3.8	1276	4	US-09-982-610-24	Sequence 24, Appl
660	64	3.8	1276	5	PCT-US95-04228-24	Sequence 10, Appl
661	64	3.8	1984	3	US-08-836-325-10	Sequence 10, Appl
662	64	3.8	1984	4	US-09-457-571-10	Sequence 9, Appli
663	63.5	3.7	199	3	US-08-737-248-9	Sequence 6759, Ap
664	63.5	3.7	226	4	US-09-107-532A-6759	Sequence 2, Appli
665	63.5	3.7	243	2	US-08-771-455-2	Sequence 2, Appli
666	63.5	3.7	262	3	US-08-889-425-2	Sequence 6754, Ap
667	63.5	3.7	262	4	US-09-949-016-6754	Sequence 5052, Ap
668	63.5	3.7	374	4	US-09-543-681A-5052	Sequence 85, Appl
669	63.5	3.7	376	2	US-08-846-762-85	Sequence 7608, Ap
670	63.5	3.7	386	4	US-09-328-352-7608	Sequence 4894, Ap
671	63.5	3.7	419	4	US-09-107-532A-4894	Sequence 42290, A
672	63.5	3.7	435	4	US-09-270-767-42290	Patent No. 5194375
673	63.5	3.7	459	6	5194375-2	Patent No. 5194375
674	63.5	3.7	459	6	5194375-2	Patent No. 5194375
675	63.5	3.7	475	4	US-09-248-796A-14607	Sequence 14607, A
676	63.5	3.7	491	3	US-09-134-001C-4727	Sequence 4727, Ap
677	63.5	3.7	501	1	US-08-149-105-15	Sequence 15, Appl
678	63.5	3.7	501	1	US-08-317-847-15	Sequence 185, App
679	63.5	3.7	501	4	US-09-907-794A-185	Sequence 185, App
680	63.5	3.7	501	4	US-09-905-125A-185	Sequence 185, App
681	63.5	3.7	501	4	US-09-902-775A-185	Sequence 185, App
682	63.5	3.7	501	4	US-09-906-700-185	Sequence 185, App
683	63.5	3.7	501	4	US-09-903-603A-185	Sequence 185, App
684	63.5	3.7	501	4	US-09-904-920A-185	Sequence 185, App

685	63.5	3.7	501	4	US-09-909-064-185	Sequence 185, App
686	63.5	3.7	501	4	US-09-905-381A-185	Sequence 185, App
687	63.5	3.7	501	4	US-09-906-618-185	Sequence 185, App
688	63.5	3.7	502	4	US-09-252-991A-20651	Sequence 20651, A
689	63.5	3.7	505	1	US-08-220-603A-10	Sequence 10, Appl
690	63.5	3.7	522	3	US-08-821-984-10	Sequence 10, Appl
691	63.5	3.7	522	3	US-09-329-749-10	Sequence 10, Appl
692	63.5	3.7	522	4	US-09-502-264-10	Sequence 10, Appl
693	63.5	3.7	540	4	US-09-107-532A-5467	Sequence 5467, Ap
694	63.5	3.7	567	1	US-08-361-873A-2	Sequence 2, Appll
695	63.5	3.7	567	2	US-08-483-926A-1	Sequence 1, Appll
696	63.5	3.7	567	2	US-08-854-768-1	Sequence 1, Appll
697	63.5	3.7	567	2	US-08-445-520B-9	Sequence 9, Appll
698	63.5	3.7	567	2	US-08-737-045-1	Sequence 1, Appll
699	63.5	3.7	567	3	US-08-451-946B-8	Sequence 8, Appll
700	63.5	3.7	567	3	US-08-446-938B-8	Sequence 8, Appll
701	63.5	3.7	567	3	US-08-311-703A-8	Sequence 8, Appll
702	63.5	3.7	567	3	US-08-446-939B-8	Sequence 8, Appll
703	63.5	3.7	567	3	US-09-183-543-8	Sequence 8, Appll
704	63.5	3.7	567	3	US-08-446-936A-8	Sequence 8, Appll
705	63.5	3.7	567	3	US-09-239-864A-11	Sequence 11, Appl
706	63.5	3.7	567	4	US-09-878-905-11	Sequence 11, Appl
707	63.5	3.7	567	4	US-09-267-963D-36	Sequence 36, Appl
708	63.5	3.7	567	5	PCT-US92-09326-4	Sequence 4, Appll
709	63.5	3.7	572	5	PCT-US91-08177-11	Sequence 11, Appl
710	63.5	3.7	593	4	US-09-270-767-41549	Sequence 41549, A
711	63.5	3.7	661	4	US-09-540-236-3743	Sequence 3743, Ap
712	63.5	3.7	839	4	US-09-949-016-10846	Sequence 10846, A
713	63.5	3.7	871	3	US-09-245-041-19	Sequence 19, Appl
714	63.5	3.7	871	4	US-09-358-055B-19	Sequence 19, Appl
715	63.5	3.7	871	4	US-09-893-238-19	Sequence 19, Appl
716	63.5	3.7	926	1	US-08-159-340A-2	Sequence 2, Appll
717	63.5	3.7	1041	3	US-08-898-978-2	Sequence 2, Appll
718	63.5	3.7	1041	3	US-09-372-858-2	Sequence 2, Appll
719	63.5	3.7	1350	3	US-09-245-041-17	Sequence 17, Appl
720	63.5	3.7	1350	4	US-09-358-055B-17	Sequence 17, Appl
721	63.5	3.7	1350	4	US-09-893-238-17	Sequence 17, Appl
722	63.5	3.7	1391	4	US-09-538-092-250	Sequence 250, App
723	63.5	3.7	1463	1	US-08-220-603A-11	Sequence 11, Appl
724	63.5	3.7	1487	4	US-09-489-039A-12113	Sequence 12113, A
725	63.5	3.7	1956	3	US-08-843-417-2	Sequence 2, Appll
726	63.5	3.7	1956	4	US-09-527-013-2	Sequence 2, Appll
727	63.5	3.7	1957	4	US-08-669-656A-8	Sequence 8, Appll
728	63.5	3.7	2132	4	US-08-669-656A-6	Sequence 6, Appll
729	63.5	3.7	2227	4	US-10-104-966-12	Sequence 12, Appl
730	63.5	3.7	2813	3	US-08-896-449A-2	Sequence 2, Appll
731	63.5	3.7	2813	3	US-09-132-652-2	Sequence 2, Appll
732	63.5	3.7	2813	4	US-09-886-900A-2	Sequence 2, Appll
733	63.5	3.7	2813	4	US-09-662-478C-2	Sequence 2, Appll
734	63.5	3.7	3730	4	US-09-949-016-9908	Sequence 9908, Ap
735	63	3.7	166	3	US-08-916-576B-6	Sequence 6, Appll
736	63	3.7	166	4	US-10-078-337-6	Sequence 6, Appll
737	63	3.7	203	4	US-09-328-352-4293	Sequence 4293, Ap
738	63	3.7	204	4	US-09-489-039A-8937	Sequence 8937, Ap
739	63	3.7	225	4	US-09-252-991A-27421	Sequence 27421, A
740	63	3.7	259	4	US-09-328-352-4873	Sequence 4873, Ap
741	63	3.7	307	4	US-09-489-039A-8048	Sequence 8048, Ap
742	63	3.7	314	4	US-09-248-796A-14618	Sequence 14618, A
743	63	3.7	320	4	US-09-949-016-6587	Sequence 6587, Ap
744	63	3.7	323	4	US-09-489-039A-8083	Sequence 8083, Ap
745	63	3.7	331	4	US-09-270-767-41873	Sequence 41873, A
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747	63	3.7	335	3	US-08-442-108B-23	Sequence 23, Appl
748	63	3.7	335	4	US-09-543-681A-4369	Sequence 4369, Ap
749	63	3.7	384	4	US-09-152-060-118	Sequence 118, App
750	63	3.7	385	4	US-09-198-452A-976	Sequence 976, App
751	63	3.7	391	4	US-09-438-185A-905	Sequence 905, App
752	63	3.7	393	4	US-09-634-238-274	Sequence 274, App
753	63	3.7	398	4	US-09-489-039A-10213	Sequence 10213, A
754	63	3.7	413	3	US-09-134-001C-4058	Sequence 4058, Ap
755	63	3.7	485	4	US-09-949-016-10882	Sequence 10882, A
756	63	3.7	488	4	US-09-949-016-9120	Sequence 9120, Ap
757	63	3.7	551	4	US-09-543-681A-4462	Sequence 4462, Ap
758	63	3.7	552	3	US-08-851-843A-4	Sequence 4, Appll
759	63	3.7	552	3	US-08-854-050-4	Sequence 4, Appll
760	63	3.7	552	3	US-09-430-323-4	Sequence 4, Appll
761	63	3.7	552	4	US-09-766-253-4	Sequence 4, Appll
762	63	3.7	562	6	5258502-2	Patent No. 5258502
763	63	3.7	562	6	5258502-2	Patent No. 5258502
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765	63	3.7	621	4	US-09-949-016-11582	Sequence 11582, A
766	63	3.7	638	4	US-09-902-540-11575	Sequence 11575, A
767	63	3.7	641	1	US-08-441-139-4	Sequence 4, Appll
768	63	3.7	746	4	US-09-248-796A-15023	Sequence 15023, A
769	63	3.7	756	4	US-09-248-796A-14736	Sequence 14736, A
770	63	3.7	770	1	US-08-369-796-12	Sequence 12, Appl
771	63	3.7	770	2	US-08-852-091-12	Sequence 12, Appl
772	63	3.7	770	2	US-08-820-754-12	Sequence 12, Appl
773	63	3.7	770	3	US-08-956-652-12	Sequence 12, Appl
774	63	3.7	770	3	US-08-956-869-12	Sequence 12, Appl
775	63	3.7	770	3	US-08-948-547-12	Sequence 12, Appl
776	63	3.7	770	3	US-09-364-970-3	Sequence 3, Appll
777	63	3.7	770	3	US-09-364-970-5	Sequence 5, Appll
778	63	3.7	770	3	US-08-956-653A-12	Sequence 12, Appl
779	63	3.7	770	4	US-08-212-185-12	Sequence 12, Appl
780	63	3.7	770	5	PCT-US95-17025-12	Sequence 12, Appl
781	63	3.7	787	4	US-09-825-294-207	Sequence 207, App
782	63	3.7	787	4	US-09-970-966-207	Sequence 207, App
783	63	3.7	793	4	US-09-313-942-32	Sequence 32, Appl
784	63	3.7	801	4	US-09-248-796A-18375	Sequence 18375, A
785	63	3.7	846	3	US-08-885-291-55	Sequence 55, Appl
786	63	3.7	846	3	US-09-107-847-2	Sequence 2, Appll
787	63	3.7	846	3	US-09-496-672-55	Sequence 55, Appl
788	63	3.7	851	1	US-08-369-796-2	Sequence 2, Appll
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790	63	3.7	851	2	US-08-820-754-2	Sequence 2, Appll
791	63	3.7	851	3	US-08-956-652-2	Sequence 2, Appll
792	63	3.7	851	3	US-08-956-869-2	Sequence 2, Appll
793	63	3.7	851	3	US-09-012-710-2	Sequence 2, Appll
794	63	3.7	851	3	US-08-948-547-2	Sequence 2, Appll
795	63	3.7	851	3	US-09-087-465-4	Sequence 4, Appll
796	63	3.7	851	3	US-09-364-970-2	Sequence 2, Appll
797	63	3.7	851	3	US-09-556-273-2	Sequence 2, Appll
798	63	3.7	851	3	US-08-956-653A-2	Sequence 2, Appll
799	63	3.7	851	4	US-09-972-800A-4	Sequence 4, Appll
800	63	3.7	851	4	US-08-212-185-2	Sequence 2, Appll
801	63	3.7	851	5	PCT-US95-17025-2	Sequence 2, Appll
802	63	3.7	852	1	US-08-276-099A-13	Sequence 13, Appl
803	63	3.7	852	1	US-08-781-890-13	Sequence 13, Appl
804	63	3.7	856	4	US-09-152-060-77	Sequence 77, Appl
805	63	3.7	939	4	US-09-248-796A-16082	Sequence 16082, A
806	63	3.7	1014	4	US-10-101-464A-807	Sequence 807, App
807	63	3.7	1045	4	US-09-949-016-11112	Sequence 11112, A
808	63	3.7	1151	4	US-09-023-905A-4	Sequence 4, Appll
809	63	3.7	1162	2	US-08-599-455B-43	Sequence 43, Appl
810	63	3.7	1162	3	US-09-069-781B-43	Sequence 43, Appl
811	63	3.7	1162	3	US-09-137-132-43	Sequence 43, Appl
812	63	3.7	1162	3	US-08-864-564A-43	Sequence 43, Appl
813	63	3.7	1162	4	US-09-094-410-43	Sequence 43, Appl
814	63	3.7	1162	4	US-08-708-123D-43	Sequence 43, Appl
815	63	3.7	1162	4	US-08-638-524B-43	Sequence 43, Appl
816	63	3.7	1172	1	US-08-313-288B-19	Sequence 19, Appl
817	63	3.7	1172	4	US-09-949-016-6333	Sequence 6333, Ap
818	63	3.7	1179	4	US-09-949-016-10545	Sequence 10545, A
819	63	3.7	1453	1	US-08-308-872B-6	Sequence 6, Appll
820	63	3.7	1493	3	US-09-423-890-8	Sequence 8, Appll
821	63	3.7	1593	3	US-08-628-829-4	Sequence 4, Appll
822	63	3.7	2362	1	US-09-508-836A-8	Sequence 8, Appll
823	63	3.7	3056	2	US-08-629-001A-3	Sequence 3, Appll
824	63	3.7	3056	3	US-08-642-274D-3	Sequence 3, Appll
825	63	3.7	3056	3	US-08-952-127-3	Sequence 3, Appll
826	63	3.7	3056	3	US-08-952-127-3	Sequence 3, Appll
827	63	3.7	3056	3	US-08-952-127-3	Sequence 3, Appll
828	63	3.7	4544	1	US-08-469-486-52	Sequence 52, Appl
829	63	3.7	4544	2	US-08-469-486-52	Sequence 52, Appl
830	62.5	3.7	151	4	US-09-270-767-37639	Sequence 37639, A

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832	62.5	3.7	176	4	US-09-328-352-5939	Sequence 5939, Ap	905	62.5	3.7	1454	5	PCT-US91-08525-26	Sequence 26, Appl
833	62.5	3.7	180	4	US-09-328-352-6739	Sequence 6739, Ap	906	62.5	3.7	1454	5	PCT-US93-04384-8	Sequence 8, Appl
834	62.5	3.7	191	4	US-09-621-976-4640	Sequence 4640, Ap	907	62.5	3.7	1827	4	US-09-443-780C-14	Sequence 14, Appl
835	62.5	3.7	205	4	US-09-248-796A-22069	Sequence 22069, A	908	62.5	3.7	1827	4	US-09-079-723-179	Sequence 179, App
836	62.5	3.7	286	4	US-09-248-796A-22818	Sequence 22818, A	909	62.5	3.7	2475	3	US-09-413-814-48	Sequence 48, Appl
837	62.5	3.7	288	4	US-09-270-767-35019	Sequence 35019, A	910	62.5	3.7	2492	4	US-09-991-258-3	Sequence 3, Appl
838	62.5	3.7	288	4	US-09-270-767-50236	Sequence 50236, A	911	62.5	3.7	2710	1	US-08-480-604A-6	Sequence 6, Appl
839	62.5	3.7	291	4	US-09-393-634-64	Sequence 64, Appl	912	62.5	3.7	2710	2	US-08-405-496A-6	Sequence 6, Appl
840	62.5	3.7	291	4	US-09-949-016-6919	Sequence 6919, Ap	913	62.5	3.7	2710	3	US-08-915-136-6	Sequence 6, Appl
841	62.5	3.7	291	4	US-09-949-016-8213	Sequence 8213, Ap	914	62.5	3.7	2710	3	US-08-957-310-6	Sequence 6, Appl
842	62.5	3.7	322	4	US-09-270-767-42152	Sequence 42152, A	915	62.5	3.7	2710	4	US-10-011-366-6	Sequence 6, Appl
843	62.5	3.7	359	4	US-09-646-028-16	Sequence 16, Appl	916	62.5	3.7	2710	4	US-09-084-517-6	Sequence 6, Appl
844	62.5	3.7	375	4	US-09-538-092-159	Sequence 159, App	917	62.5	3.7	4861	4	US-09-919-497-70	Sequence 70, Appl
845	62.5	3.7	400	4	US-09-668-097A-16	Sequence 16, Appl	918	62	3.7	174	4	US-09-489-039A-10650	Sequence 10650, A
846	62.5	3.7	411	4	US-09-253-701-1	Sequence 1, Appl	919	62	3.7	185	4	US-09-248-796A-20264	Sequence 20264, A
847	62.5	3.7	412	4	US-09-646-403-5	Sequence 5, Appl	920	62	3.7	200	4	US-09-107-532A-5545	Sequence 5545, Ap
848	62.5	3.7	437	3	US-08-486-099-91	Sequence 91, Appl	921	62	3.7	251	2	US-08-665-647-7	Sequence 7, Appl
849	62.5	3.7	437	3	US-08-360-107A-101	Sequence 101, App	922	62	3.7	267	4	US-09-489-039A-9036	Sequence 9036, Ap
850	62.5	3.7	437	3	US-08-484-223B-91	Sequence 91, Appl	923	62	3.7	282	3	US-08-812-586-49	Sequence 49, Appl
851	62.5	3.7	437	3	US-08-919-597-91	Sequence 91, Appl	924	62	3.7	282	4	US-09-535-832A-46	Sequence 46, Appl
852	62.5	3.7	437	3	US-08-475-668A-91	Sequence 91, Appl	925	62	3.7	293	2	US-08-919-145-2	Sequence 2, Appl
853	62.5	3.7	437	3	US-08-485-551A-91	Sequence 91, Appl	926	62	3.7	293	3	US-09-344-889-2	Sequence 2, Appl
854	62.5	3.7	437	3	US-08-471-913A-91	Sequence 91, Appl	927	62	3.7	308	2	US-09-047-026A-23	Sequence 23, Appl
855	62.5	3.7	437	3	US-08-485-264A-91	Sequence 91, Appl	928	62	3.7	341	4	US-09-399-081A-6	Sequence 6, Appl
856	62.5	3.7	437	3	US-08-474-349A-91	Sequence 91, Appl	929	62	3.7	347	4	US-09-248-796A-19101	Sequence 19101, A
857	62.5	3.7	437	4	US-08-255-208A-27	Sequence 27, Appl	930	62	3.7	378	2	US-08-904-031-4	Sequence 4, Appl
858	62.5	3.7	437	4	US-08-470-896-91	Sequence 91, Appl	931	62	3.7	385	4	US-09-248-796A-14377	Sequence 14377, A
859	62.5	3.7	437	4	US-08-485-546A-91	Sequence 91, Appl	932	62	3.7	386	4	US-09-949-016-10095	Sequence 10095, A
860	62.5	3.7	437	4	US-08-487-266A-91	Sequence 2, Appl	933	62	3.7	407	4	US-09-521-335-13	Sequence 13, Appl
861	62.5	3.7	449	4	US-09-984-880-2	Sequence 2, Appl	934	62	3.7	414	4	US-09-107-433-3327	Sequence 3327, Ap
862	62.5	3.7	449	4	US-10-277-032-2	Sequence 18, Appl	935	62	3.7	422	4	US-09-489-039A-12413	Sequence 12413, A
863	62.5	3.7	453	1	US-08-417-330A-18	Sequence 126, App	936	62	3.7	423	4	US-09-824-551-2	Sequence 2, Appl
864	62.5	3.7	498	4	US-09-438-185A-126	Sequence 26, Appl	937	62	3.7	427	3	US-08-969-125-9	Sequence 9, Appl
865	62.5	3.7	513	5	PCT-US91-02714-26	Sequence 19, Appl	938	62	3.7	427	4	US-09-545-002-9	Sequence 9, Appl
866	62.5	3.7	572	5	PCT-US91-08177-19	Sequence 4, Appl	939	62	3.7	427	4	US-09-949-016-6094	Sequence 6094, Ap
867	62.5	3.7	574	4	US-09-567-458A-4	Sequence 4, Appl	940	62	3.7	443	3	US-09-155-855-1	Sequence 1, Appl
868	62.5	3.7	574	6	5223254-2	Sequence 6, Appl	941	62	3.7	443	3	US-09-155-855-2	Sequence 2, Appl
869	62.5	3.7	574	6	5223254-2	Sequence 6, Appl	942	62	3.7	443	3	US-09-543-744-1	Sequence 1, Appl
870	62.5	3.7	613	4	US-09-438-833-6	Sequence 6213, Ap	943	62	3.7	443	3	US-09-543-744-2	Sequence 2, Appl
871	62.5	3.7	626	4	US-09-949-016-6213	Sequence 4304, Ap	944	62	3.7	443	4	US-09-929-060-1	Sequence 1, Appl
872	62.5	3.7	639	4	US-09-107-532A-4304	Sequence 17974, A	945	62	3.7	443	4	US-09-929-060-2	Sequence 2, Appl
873	62.5	3.7	641	4	US-09-248-796A-17974	Sequence 7850, Ap	946	62	3.7	446	4	US-09-902-540-13447	Sequence 13447, A
874	62.5	3.7	664	4	US-09-949-016-7850	Sequence 28, Appl	947	62	3.7	467	3	US-09-155-855-3	Sequence 3, Appl
875	62.5	3.7	688	1	US-07-688-352C-28	Sequence 28, Appl	948	62	3.7	467	3	US-09-543-744-3	Sequence 3, Appl
876	62.5	3.7	688	2	US-08-474-379C-28	Sequence 28, Appl	949	62	3.7	467	4	US-09-929-060-3	Sequence 3, Appl
877	62.5	3.7	688	3	US-09-146-249A-28	Sequence 28, Appl	950	62	3.7	468	4	US-09-149-476-387	Sequence 387, App
878	62.5	3.7	688	3	US-08-206-188B-28	Sequence 28, Appl	951	62	3.7	469	4	US-09-252-991A-30596	Sequence 30596, A
879	62.5	3.7	716	2	US-08-372-652-4	Sequence 4, Appl	952	62	3.7	477	4	US-09-543-681A-8129	Sequence 8129, Ap
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881	62.5	3.7	807	4	US-09-132-769-3	Sequence 9, Appl	954	62	3.7	489	4	US-09-134-000C-4888	Sequence 4888, Ap
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883	62.5	3.7	905	3	US-09-357-014-9	Sequence 8, Appl	956	62	3.7	549	4	US-09-673-395A-208	Sequence 208, App
884	62.5	3.7	920	3	US-08-930-996A-8	Sequence 11808, A	957	62	3.7	549	4	US-09-673-395A-564	Sequence 564, App
885	62.5	3.7	1011	4	US-09-489-039A-11808	Sequence 8, Appl	958	62	3.7	571	4	US-09-248-796A-22498	Sequence 22498, A
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890	62.5	3.7	1091	6	5516630-2	Patent No. 5516630	963	62	3.7	579	4	US-10-115-671-19	Sequence 19, Appl
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892	62.5	3.7	1101	3	US-08-331-625A-52	Sequence 52, Appl	965	62	3.7	580	4	US-09-254-590-2	Sequence 2, Appl
893	62.5	3.7	1101	3	US-09-494-151-52	Sequence 52, Appl	966	62	3.7	580	4	US-10-115-415-2	Sequence 2, Appl
894	62.5	3.7	1101	4	US-09-972-484-52	Sequence 52, Appl	967	62	3.7	580	4	US-10-115-260-2	Sequence 2, Appl
895	62.5	3.7	1166	4	US-10-101-464A-900	Sequence 900, App	968	62	3.7	580	4	US-10-115-671-2	Sequence 2, Appl
896	62.5	3.7	1383	4	US-09-540-236-3580	Sequence 3580, App	969	62	3.7	592	2	US-08-366-490-2	Sequence 2, Appl
897	62.5	3.7	1443	1	US-08-308-872B-2	Sequence 2, Appl	970	62	3.7	592	3	US-08-860-483A-2	Sequence 2, Appl
898	62.5	3.7	1452	3	US-08-331-625A-2	Sequence 2, Appl	971	62	3.7	600	4	US-09-519-232-20	Sequence 20, Appl
899	62.5	3.7	1452	3	US-09-494-151-2	Sequence 2, Appl	972	62	3.7	601	4	US-09-519-232-72	Sequence 72, Appl
900	62.5	3.7	1452	4	US-09-972-484-2	Sequence 2, Appl	973	62	3.7	604	4	US-09-134-000C-5256	Sequence 5256, Ap
901	62.5	3.7	1452	5	PCT-US93-04384-18	Sequence 18, Appl	974	62	3.7	609	4	US-09-949-016-7747	Sequence 7747, Ap
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978	62	3.7	609	4	US-09-949-016-7751	Sequence 7751, Ap	1051	61.5	3.6	734	1	US-08-276-099A-16	Sequence 16, Appl
979	62	3.7	609	4	US-09-949-016-7752	Sequence 7752, Ap	1052	61.5	3.6	734	1	US-08-781-890-16	Sequence 16, Appl
980	62	3.7	609	4	US-09-949-016-7753	Sequence 7753, Ap	1053	61.5	3.6	738	4	US-09-107-532A-5096	Sequence 5096, Ap
981	62	3.7	609	4	US-09-949-016-7754	Sequence 7754, Ap	1054	61.5	3.6	820	4	US-09-248-796A-15055	Sequence 15055, A
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984	62	3.7	708	4	US-09-443-780C-16	Sequence 16, Appl	1057	61.5	3.6	897	4	US-09-849-602-18	Sequence 18, Appl
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998	62	3.7	1139	3	US-09-113-825-4	Sequence 4, Appli	1071	61.5	3.6	1989	3	US-09-457-571-12	Sequence 12, Appl
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1018	61.5	3.6	90	2	US-08-319-052-5	Sequence 5, Appli	1091	61	3.6	167	4	US-09-492-709A-345	Sequence 345, App
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1021	61.5	3.6	119	4	US-09-253-794-10	Sequence 10, Appl	1094	61	3.6	198	4	US-09-513-999C-5428	Sequence 5428, Ap
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1037	61.5	3.6	500	2	US-08-987-519-1	Sequence 1, Appli	1110	61	3.6	274	4	US-09-312-283C-336	Sequence 336, App
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1128	61	3.6	387	3	US-08-479-869-7	Sequence 7, Appli
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1193	61	3.6	807	4	US-09-713-550-186	Sequence 186, App
1194	61	3.6	807	4	US-09-825-294-186	Sequence 186, App
1195	61	3.6	807	4	US-09-970-966-186	Sequence 186, App
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1198	61	3.6	860	4	US-07-945-295-4	Sequence 4, Appli
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1202	61	3.6	879	4	US-09-214-259-38	Sequence 38, Appli
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1279	60.5	3.6	688	1	US-08-454-439-19	Sequence 19, Appl	1352	60	3.5	122	4	US-09-513-999C-8116	Sequence 8116, Ap
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1316	60.5	3.6	1939	4	US-09-854-856-32	Sequence 32, Appl	1389	60	3.5	331	2	US-09-215-087-1	Sequence 1, Appli
1317	60.5	3.6	1999	4	US-09-854-856-16	Sequence 16, Appl	1390	60	3.5	331	2	US-09-391-959-1	Sequence 1, Appli
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1424	60	3.5	574	1	US-08-312-648-2	Sequence 2, Appli
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1428	60	3.5	592	3	US-08-860-483A-6	Sequence 6, Appli
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1440	60	3.5	750	4	US-09-949-016-6791	Sequence 6791, Ap
1441	60	3.5	750	4	US-09-949-016-6792	Sequence 6792, Ap
1442	60	3.5	750	4	US-09-949-016-6793	Sequence 6793, Ap
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1447	60	3.5	875	1	US-08-250-847B-10	Sequence 10, Appl
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1449	60	3.5	875	3	US-08-464-410A-10	Sequence 10, Appl
1450	60	3.5	875	5	PCT-US94-06066-10	Sequence 10, Appl
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1452	60	3.5	1005	4	US-09-134-000C-6322	Sequence 6322, Ap
1453	60	3.5	1065	3	US-08-630-172-9	Sequence 9, Appli
1454	60	3.5	1065	3	US-09-375-419-9	Sequence 9, Appli
1455	60	3.5	1083	4	US-09-328-352-5493	Sequence 5493, Ap
1456	60	3.5	1142	2	US-08-993-118-7	Sequence 7, Appli
1457	60	3.5	1142	3	US-08-845-528C-7	Sequence 7, Appli
1458	60	3.5	1142	4	US-09-066-281B-7	Sequence 7, Appli
1459	60	3.5	1142	4	US-09-468-433C-7	Sequence 7, Appli
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1463	60	3.5	1656	4	US-09-949-016-7247	Sequence 7247, Ap
1464	60	3.5	1821	4	US-09-949-016-5938	Sequence 5938, Ap
1465	60	3.5	1969	4	US-09-418-710-72	Sequence 72, Appl
1466	60	3.5	1969	4	US-09-839-479-71	Sequence 71, Appl
1467	60	3.5	1972	4	US-09-418-710-21	Sequence 21, Appl
1468	60	3.5	1972	4	US-09-839-479-21	Sequence 21, Appl
1469	60	3.5	2411	3	US-09-268-347-36	Sequence 36, Appl
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1471	60	3.5	3969	3	US-08-061-376-5	Sequence 5, Appli
1472	60	3.5	3969	4	US-09-538-092-1262	Sequence 1262, Ap
1473	59.5	3.5	64	4	US-09-248-796A-23682	Sequence 23682, A
1474	59.5	3.5	119	2	US-08-318-157B-15	Sequence 15, Appl
1475	59.5	3.5	119	4	US-09-253-794-15	Sequence 15, Appl
1476	59.5	3.5	150	4	US-09-248-796A-25264	Sequence 25264, A
1477	59.5	3.5	202	4	US-09-248-796A-26605	Sequence 26605, A
1478	59.5	3.5	226	4	US-09-248-796A-14964	Sequence 14964, A
1479	59.5	3.5	246	4	US-09-532-856-4	Sequence 4, Appli
1480	59.5	3.5	246	4	US-09-524-100C-4	Sequence 4, Appli
1481	59.5	3.5	246	4	US-10-212-507-4	Sequence 4, Appli
1482	59.5	3.5	249	4	US-09-134-000C-4676	Sequence 4676, Ap
1483	59.5	3.5	272	4	US-09-686-583B-2	Sequence 2, Appli
1484	59.5	3.5	274	6	5489533-2	Patent No. 5489533
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1486	59.5	3.5	274	6	5489533-2	Patent No. 5489533
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1488	59.5	3.5	299	4	US-09-248-796A-15636	Sequence 15636, A
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1490	59.5	3.5	311	4	US-09-949-016-10224	Sequence 10224, A
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1497	59.5	3.5	325	3	US-09-209-605-8	Sequence 8, Appli
1498	59.5	3.5	328	4	US-09-270-767-44241	Sequence 44241, A
1499	59.5	3.5	334	4	US-09-535-909-6	Sequence 6, Appli
1500	59.5	3.5	342	4	US-09-248-796A-15115	Sequence 15115, A

ALIGNMENTS

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RESULT 1
US-09-976-594-818
; Sequence 818, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 818
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2454013CD1
US-09-976-594-818
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Query Match 100.0%; Score 1694; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 7.3e-182;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	181	QSKPEIQYAPHLEQPTNLRESSLSKMSYLOMNSQAHNRFLEDESDGFLRCLSLNSGW	240
QY	241	ILTTTLVLSVMVLIMICCATVATAVEQYVSEKLSITYGDLEFPMNEQKLNRYPASSLVVR	300
DB	241	ILTTTLVLSVMVLIMICCATVATAVEQYVSEKLSITYGDLEFPMNEQKLNRYPASSLVVR	300
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RESULT 2
US-09-149-476-476

; Sequence 476, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23


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: EARLIER FILING DATE: 1997-05-23
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: EARLIER APPLICATION NUMBER: 60/047, 501
: EARLIER FILING DATE: 1997-05-23
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: EARLIER FILING DATE: 1997-08-22
: EARLIER APPLICATION NUMBER: 60/048, 964
: EARLIER FILING DATE: 1997-06-06
: EARLIER APPLICATION NUMBER: 60/057, 650
: EARLIER FILING DATE: 1997-09-05
: EARLIER APPLICATION NUMBER: 60/056, 884
: EARLIER FILING DATE: 1997-08-22
: EARLIER APPLICATION NUMBER: 60/057, 669
: EARLIER FILING DATE: 1997-09-05
: EARLIER APPLICATION NUMBER: 60/049, 610
: EARLIER FILING DATE: 1997-06-13
: EARLIER APPLICATION NUMBER: 60/061, 060
: EARLIER FILING DATE: 1997-10-02

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; Sequence 4172, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
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; LOCATION: -31...-1
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; OTHER INFORMATION: seq LLLLTWALGSSG/TA
US-09-513-999C-4172

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RESULT 4
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; Sequence 11519, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; ORGANISM: Homo sapiens
US-09-907-794A-34

Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

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QY 116 GCQON-----QLPFAELRQELMSLMPKMHLLPPLTLVRSFMSMDMSAQ 160
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QY 161 FITSSWTFYLQADGKIIVFQSKPE-----IQYAPHLQEPNTLRESSLSKNSYLQMRN 214
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RESULT 7

US-09-905-125A-34
; Sequence 34, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-34

Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

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DB 479 GKTCAKLDSCALGD-----HGCE-----HSCVSSSEDSFVCQCFEGYILREDGKTCRKDV 528
QY 80 CQFVDDGIDLNRKLEGEESACTEAYSQSDEQYAC-----HL 115
DB 529 CQALDHG-----CEHICV-----NSDDSYTCECLEGFRLAEDGKCRKRDVCKSTHH 575


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; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-906-700-34

Query Match      5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;
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RESULT 10
US-09-903-603A-34
; Sequence 34, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Paoni, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-603A-34
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Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

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Db 479 GKTCAKLDSALGD-----HGCE-----HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDV 528
QY 80 CQFVDDGIDLNRKTKLCEESACTEAYSQSDEQYAC-----HL 115
Db 529 CQAI DHG-----CEHICV-----NSDSTYCECELEGFRLAEDGKRCRCKDVCKSTHH 575
QY 116 GCQN-----QLPFAELRQELMSLMPKMHLLPPLTLVRSFWSMDMDSAQS 160
Db 576 GCEHICVNNNGNSYICKSGEFLAEDGRCKKCTEGPIDLVFVIDGSKSLGSENFERYKQ 635
QY 161 FITSSWTFYLLQADDGKIIVFQSKPE-----IQYAPHLEQEPNLRSSLSKMYLQMRN 214
Db 636 FVT-----GIDSLTISPKARVGLQYSTQVHTFT-LRNFNSAK-----DMKK 679
QY 215 SOAHRNFLDEGSDG-----FLRCLSLNSGWILTTVLVSVWLWICCATVATAVEQY 268
Db 680 AVAHMKYMGKSGMTGLAKHMFERSFTQEG-----ARPLSTR 717
QY 269 VPSEKLSIYGD-----LEPMNEQKLNRYPASSLVVRSKTEDEHBEAGPLPTKYNLAHS 321
Db 718 VPRRAI-VFTDGRAQDDVSEWASKAKANGITMYAVGVKAIEELQEIASEPTNKHLLFYA 776
QY 322 E 322
Db 777 E 777
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RESULT 11
US-09-904-920A-34
; Sequence 34, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
```

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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
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; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-920A-34
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Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

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QY 31 GTASAEAFDSVLGDTASCHRAQOLTYPLHTYPKBEELYACQ-----RGCRLFESI 79
Db 479 GKTCAKLDSALGD-----HGCE-----HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDV 528
QY 80 CQFVDDGIDLNRKTKLCEESACTEAYSQSDEQYAC-----HL 115
Db 529 CQAI DHG-----CEHICV-----NSDSTYCECELEGFRLAEDGKRCRCKDVCKSTHH 575
QY 116 GCQN-----QLPFAELRQELMSLMPKMHLLPPLTLVRSFWSMDMDSAQS 160
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Db 576 GCEHICVNNNGNSYICKSEGFVLAEDGRCKCKTEGPIDLVFVIDGSKSLGEENFEVVKQ 635
QY 161 FITSSWTFYLAQADGKIIVFQSKPE-----IQYAPHLEQEPNTNLRSSLSKMSYLOMRN 214
Db 636 FVT-----GIIDSLTISPKARVGLQYSTQVHTEFT-LRNFNLSAK----DMKK 679
QY 215 SOAHNFLEDESDG-----FLRCLSLNSGWLITTLVLSVWVLLMICATVATAVEQY 268
Db 680 AVAHMKYMGKSGMTGLALKHMFERSFTQEG-----ARPLSTR 717
QY 269 VPSEKLSIYGD-----LEFMEQKLNRYPASSLVVVRSKTEDEHBEAGPLPTKXNLNLS 321
Db 718 VPRAAI-VFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEBELQEIASEPTNKLFPYA 776
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Db 777 E 777

RESULT 12

US-09-909-064-34
; Sequence 34, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-064-34

Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

QY 31 GTASAEAFDSVLGDTASCHRAQCLTYPLHTYKKEELYACQ-----RCGRLESI 79
Db 479 GKTCAKLDSALGD-----HGCE-----HSCVSSSEDSFVCCQCFEGYILREDGKTCRKDV 528
QY 80 CQFVDDGIDLNRKLECESACTEAYSQSDEQYAC-----HL 115
Db 529 CQALDHG-----CEHICV-----NSDSTYCECLGFRLEADGKCRKRDVCKSTHH 575
QY 116 GCQN-----QLPFAELROQLMSLMPKHLFPPLTLVRSFWSMDMSAQS 160
Db 576 GCEHICVNNNGNSYICKSEGFVLAEDGRCKCKTEGPIDLVFVIDGSKSLGEENFEVVKQ 635
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Db 636 FVT-----GIIDSLTISPKARVGLQYSTQVHTEFT-LRNFNLSAK----DMKK 679
QY 215 SOAHNFLEDESDG-----FLRCLSLNSGWLITTLVLSVWVLLMICATVATAVEQY 268
Db 680 AVAHMKYMGKSGMTGLALKHMFERSFTQEG-----ARPLSTR 717
QY 269 VPSEKLSIYGD-----LEFMEQKLNRYPASSLVVVRSKTEDEHBEAGPLPTKXNLNLS 321
Db 718 VPRAAI-VFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEBELQEIASEPTNKLFPYA 776
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Db 777 E 777

RESULT 13

US-09-905-381A-34
; Sequence 34, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.

```

; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; PRIOR APPLICATION NUMBER: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-905-381A-34

Query Match      5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;

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QY      161 FITSSWTFYLOADDGKIVIFQSKPE-----IOYAPHLQEPNTNRESSLSKMSYLOMRN 214
      |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      636 FVT-----GILDSLITSPKARVGLQYSTQVHTEFT-LRNFNNAK-----DMKK 679

QY      215 SOAHNPFLEDESDG-----FLRCLSLNSGWIITTTVLVSWMLWICATVATAVEQY 268
      |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      680 AVAHMKYMGKGSMTGLALKHMFERSFTQGE-----ARPLSTR 717

QY      269 VPSEKLSIYGD-----LEFMNEQKLNRYPASSLVVRSKTEDHEEAGPLPTKVNLAHS 321
      |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      718 VPRAAI-VFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEEELQETIASSEPTNKLFFYA 776

QY      322 E 322
      |
Db      777 E 777

RESULT 14
US-09-906-618-34
; Sequence 34, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; PRIOR APPLICATION NUMBER: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
```



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/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 34
/ LENGTH: 915
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-906-618-34
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Best Local Similarity 18.0%; Pred. No. 0.29;
Matches 65; Conservative 47; Mismatches 118; Indels 131; Gaps 15;
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QY 31 GTASAEAFDSVLGDTASCHRAQCLTYPLHTYPEEELYACQ-----RGCRLFSI 79
Db 479 GKTCAKLDSALGD-----HGCE-----HSCVSSSEDSFVCQCEGYILREDGKTCRRKV 528
QY 80 CQFVDDGIDLNRKLECESACTEAYSQSDEQYAC-----HL 115
Db 529 CQALDHG-----CEHICV-----NSDSDSYCECELEGFRLAEDGKRCRKDVCKSTH 575
QY 116 GCQN-----QLPFAELRQELMSLMPKHLFPPLTLVRSFWSMDMSAQS 160
Db 576 GCEHICVNNGNSYICKSEGFVLAEDGRCKCTEGPIDLVFVIDGSKSLGSENFVVKQ 635
QY 161 FITSSWTFYLQADDGKIYIFOSKPE-----IQYAPHLQEPNTLRESSLKMSYLOMEN 214
Db 636 FVT-----GILDSLITSPKARVGLQYSTQVHTEFT-LRNFNLSAK---DMKK 679
QY 215 SQAHNPLEDESDG-----FLRCLSLNSGWILTTVLVSVMLWICCATVATAVEQY 268
Db 680 AVAHMKYMGKSGMTGLALKMFERSFTQEG-----ARPLSTR 717
QY 269 VPSEKLSIYGD-----LEFMNEQKLNRYPASSLVVRSKTEDHEAGPLPTKYNLAHS 321
Db 718 VPRAAI-VFTDGRAQDDVSEWASKAKANGITMYAVGVGAIEBELQEIASEPTNKHLFYA 776
QY 322 E 322
Db 777 E 777
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RESULT 15
US-09-949-016-6215
Sequence 6215, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0

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/ SEQ ID NO 6215
/ LENGTH: 956
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-6215
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Query Match      5.5%; Score 93.5; DB 4; Length 956;
Best Local Similarity 18.0%; Pred. No. 0.53;
Matches 65; Conservative 46; Mismatches 119; Indels 131; Gaps 15;
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QY 31 GTASAEAFDSVLGDTASCHRAQCLTYPLHTYPEEELYACQ-----RGCRLFSI 79
Db 520 GKTCAKLDSALGD-----HGCE-----HSCVSSSEDSFVCQCEGYILREDGKTCRRKV 569
QY 80 CQFVDDGIDLNRKLECESACTEAYSQSDEQYAC-----HL 115
Db 570 CQALDHG-----CEHICV-----NSDSDSYCECELEGFRLAEDGKRCRKDVCKSTH 616
QY 116 GCQN-----QLPFAELRQELMSLMPKHLFPPLTLVRSFWSMDMSAQS 160
Db 617 GCEHICVNNGNSYICKSEGFVLAEDGRCKCTEGPIDLVFVIDGSKSLGSENFVVKQ 676
QY 161 FITSSWTFYLQADDGKIYIFOSKPE-----IQYAPHLQEPNTLRESSLKMSYLOMEN 214
Db 677 FVT-----GILDSLITSPKARVGLQYSTQVHTEFT-LRNFNLSAK---DMKK 720
QY 215 SQAHNPLEDESDG-----FLRCLSLNSGWILTTVLVSVMLWICCATVATAVEQY 268
Db 721 AVAHMKYMGKSGMTGLALKMFERSFTQEG-----ARPFSTR 758
QY 269 VPSEKLSIYGD-----LEFMNEQKLNRYPASSLVVRSKTEDHEAGPLPTKYNLAHS 321
Db 759 VPRAAI-VFTDGRAQDDVSEWASKAKANGITMYAVGVGAIEBELQEIASEPTNKHLFYA 817
QY 322 E 322
Db 818 E 818
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Search completed: March 28, 2005, 13:10:28
Job time : 41 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: March 28, 2005, 13:08:15 ; Search time 68 Seconds
(without alignments)

1837.112 Million cell updates/sec

Title: US-09-978-299A-330

Perfect score: 1694

Sequence: 1 MAAPKSLWVRIGLHPPL.....EDHEAGPLPTKVNLAHSEI 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
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RESULT 1

ID AAY41733 standard; protein; 323 AA.

DE Human PRO195 protein sequence.

PN WO946281-A2.

PD 16-SEP-1999.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 2; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 2

ID AAY57939 standard; protein; 323 AA.

DE Human transmembrane protein HTMPN-63.

PN WO961471-A2.

PD 02-DEC-1999.

PA (INCY-) INCYTE PHARM INC.

Query Match 100.0%; Score 1694; DB 3; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 3

ID AAB44289 standard; protein; 323 AA.

DE Human PRO195 (UNQ169) protein sequence SEQ ID NO:330.

PN WO200053756-A2.

PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 3; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 4

ID AAB24394 standard; protein; 323 AA.

DE Human PRO195 protein sequence SEQ ID NO:31.

PN WO200032221-A2.

PD 08-JUN-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 3; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 5

ID AAY78804 standard; protein; 323 AA.

DE Hydrophobic domain containing protein clone HP10349 protein sequence.

PN WO20000506-A2.

PD 06-JAN-2000.

PA (SAGA) SAGAMI CHEM RES CENT.

PA (PROT-) PROTEGENE INC.

Query Match 100.0%; Score 1694; DB 3; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 6

ID AAM93600 standard; protein; 323 AA.

DE Human polypeptide, SEQ ID NO: 3412.

PN EP130094-A2.

PD 05-SEP-2001.

PA (HELI-) HELIX RES INST.

Query Match 100.0%; Score 1694; DB 4; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 7

ID AAV12307 standard; protein; 323 AA.

DE Human PRO195 polypeptide sequence.

PN WO200140466-A2.

PD 07-JUN-2001.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 4; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 8

ID AAB53073 standard; protein; 323 AA.

DE Human angiogenesis-associated protein PRO195, SEQ ID NO:46.

PN WO200053753-A2.

PD 14-SEP-2000.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 4; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 9

ID AAB88428 standard; protein; 323 AA.

DE Human membrane or secretory protein clone PSEC0203.

PN EP1067182-A2.

PD 10-JAN-2001.

PA (HELI-) HELIX RES INST.

Query Match 100.0%; Score 1694; DB 4; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 10

ID ABB84820 standard; protein; 323 AA.

DE Human PRO195 protein sequence SEQ ID NO:8.

PN WO200200690-A2.

PD 03-JAN-2002.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 5; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 11

ID ABB95426 standard; protein; 323 AA.

DE Human angiogenesis related protein PRO195 SEQ ID NO: 8.

PN WO200208284-A2.

PD 31-JAN-2002.

PA (GETH) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

Query Match 100.0%; Score 1694; DB 5; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 12

ID ABO17751 standard; protein; 323 AA.

DE Novel human secreted and transmembrane protein PRO195.

PN US2003032156-A1.

PD 13-FEB-2003.

PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1694; DB 6; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 13

ID ABO25235 standard; protein; 323 AA.

DE Novel human secreted and transmembrane protein PRO195.

PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 14
ID ABU81005 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 15
ID ABU72241 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 16
ID ABU66705 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 17
ID ABU84921 standard; protein; 323 AA.
DE Human secreted and transmembrane polypeptide PRO195.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 18
ID ABU59786 standard; protein; 323 AA.
DE Novel secreted and transmembrane protein PRO195.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 19
ID ABU6119 standard; protein; 323 AA.
DE Human PRO195 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 20
ID ABO24976 standard; protein; 323 AA.
DE Human secreted/transmembrane protein (PRO) #136.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 21
ID ABU80388 standard; protein; 323 AA.
DE Human secreted/transmembrane protein PRO195.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 22
ID ABU66981 standard; protein; 323 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 272.
PN US2003032155-A1.

PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 23
ID ADA45791 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 24
ID ADA76222 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 25
ID ADA18872 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 26
ID ADA61495 standard; protein; 323 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 27
ID ADB19280 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 28
ID ADB27821 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 29
ID ADA86300 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 30
ID ADB15864 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 31
ID ADA47650 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003073215-A1.
PD 17-APR-2003.


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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 32
ID ADA67445 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 33
ID ADB30452 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 34
ID ADA65748 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 35
ID ADA96960 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 36
ID ADA79264 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 37
ID ADA87403 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 38
ID ADB16605 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 39
ID ADA91697 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 40
ID ADB14760 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 41
ID ADA24869 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 42
ID ADB18721 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US200307722-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 43
ID ADA93936 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 44
ID ADB19832 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 45
ID ADB13144 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 46
ID ABO43284 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 47
ID ABO19690 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 48
ID ADA12530 standard; protein; 323 AA.
DE Human secreted/transmembrane polypeptide PRO195.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 49
ID ADA74398 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
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Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 50
ID ADB24631 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 51
ID ADA82155 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 52
ID ADA75118 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 53
ID ADA85196 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 54
ID ADA84644 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 55
ID ADB29900 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 56
ID ADA80428 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 57
ID ADA75670 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 58
ID ADA46895 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

RESULT 59
ID ADB25191 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 60
ID ADA93367 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 61
ID ADB26717 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 62
ID ADB31004 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 63
ID ADA60932 standard; protein; 323 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 64
ID ADB24079 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 65
ID ADA96408 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 66
ID ADA80980 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 67
ID ADA95856 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 68
ID ADA95856 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 6; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;

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ID ADB26165 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 6; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 69  
ID ADB21650 standard; protein; 323 AA.  
DE Novel human secreted and transmembrane protein PRO195.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 6; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 70  
ID ABO19581 standard; protein; 323 AA.  
DE Novel human secreted and transmembrane polypeptide #49.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 6; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 71  
ID ADA77429 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 72  
ID ADB18169 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 73  
ID ADA68652 standard; protein; 323 AA.  
DE Novel human secreted and transmembrane protein PRO195.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 74  
ID ADA87955 standard; protein; 323 AA.  
DE Novel human secreted and transmembrane protein PRO195.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 75  
ID ADA46343 standard; protein; 323 AA.  
DE Novel human secreted and transmembrane protein PRO195.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 76  
ID ADB28373 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 77  
ID ADB28925 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.
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PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 78  
ID ADA76877 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 79  
ID ADA88507 standard; protein; 323 AA.  
DE Novel human secreted and transmembrane protein PRO195.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 80  
ID ADA97512 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 81  
ID ADB27269 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 82  
ID ADB22202 standard; protein; 323 AA.  
DE Novel human secreted and transmembrane protein PRO195.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 83  
ID ADA66893 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 84  
ID ADB22754 standard; protein; 323 AA.  
DE Human PRO polypeptide #136.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 85  
ID ADB23527 standard; protein; 323 AA.  
DE Human PRO polypeptide SEQ ID NO 272.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1694; DB 7; Length 323;  
Best Local Similarity 100.0%; Pred. No. 8.4e-167;  
RESULT 86  
ID ADA92249 standard; protein; 323 AA.  
DE Novel human secreted and transmembrane protein PRO195.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 87
ID ADB15312 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 88
ID ADB38564 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 89
ID ADB38012 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 90
ID ADB66484 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 91
ID ADB89564 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 92
ID ADB90296 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 93
ID ADB39397 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 94
ID ADB73836 standard; protein; 323 AA.
DE Human PRO polypeptide #49.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 95
ID ADB47020 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;

Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 96
ID ADB86627 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 97
ID ADB76552 standard; protein; 323 AA.
DE Human PRO polypeptide #49.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 98
ID ADB77232 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 99
ID ADB34389 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 100
ID ADB35493 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 101
ID ADB33837 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 102
ID ADB34941 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 103
ID ADB36045 standard; protein; 323 AA.
DE Human PRO polypeptide SEQ ID NO 272.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 104
ID ADB46440 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;


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RESULT 105
ID ADC37345 standard; protein; 323 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 178.
PN W02003048202-A2.
PD 12-JUN-2003.
PA (ASAH ) ASAH KASEI KK.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 106
ID ADC43978 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 107
ID ADC61738 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 108
ID ADC63702 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 109
ID ADC66802 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 110
ID ADC68926 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003060407-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 111
ID ADC62986 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 112
ID ADC68051 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 113
ID ADC41371 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 114
ID ADC50866 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 115
ID ADC62362 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 116
ID ADC41995 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 117
ID ADC50313 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 118
ID ADC71860 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 119
ID ADC59839 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 120
ID ADC52846 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 121
ID ADC57200 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 122
ID ADC60391 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 123
ID ADC50866 standard; protein; 323 AA.
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DE Novel human secreted and transmembrane protein PRO195.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 124
ID ADC65393 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 125
ID ADC54491 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 126
ID ADC53452 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 127
ID ADC58975 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 128
ID ADC55853 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 129
ID ADC58423 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein Seq ID272.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 130
ID ADD03097 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 131
ID ADC90089 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 132
ID ADC69508 standard; protein; 323 AA.
DE Human PRO polypeptide #136.

PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 133
ID ADC48397 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 134
ID ADD09926 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 135
ID ADD04501 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 136
ID ADC80457 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 137
ID ADD10964 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 138
ID ADD10297 standard; protein; 323 AA.
DE Human secreted/transmembrane PRO polypeptide #4.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 139
ID ADC47845 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 140
ID ADC79905 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 141
ID ADD11257 standard; protein; 323 AA.
DE Human secreted/transmembrane PRO polypeptide #4.
PN US2003105013-A1.

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PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 142
ID ADD09374 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 143
ID ADD41087 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 144
ID ADD52226 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 145
ID ADD52966 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 146
ID ADD53518 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 147
ID ADD37050 standard; protein; 323 AA.
DE Human secreted/transmembrane PRO polypeptide #4.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 148
ID ADD51674 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 149
ID ADD02473 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 150
ID ADD01907 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 151
ID ADD54089 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 152
ID ADE49364 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 153
ID ADD92406 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 154
ID ADD91302 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 155
ID ADE03916 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 156
ID ADE32213 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 157
ID ADE22145 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 158
ID ADD79369 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 159
ID ADE35418 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
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Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 160
ID ADE16532 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 161
ID ADD73147 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 162
ID ADE41905 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 163
ID ADE17722 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 164
ID ADD91854 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 165
ID ADE33317 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 166
ID ADE33869 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 167
ID ADD79921 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 168
ID ADD92958 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
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Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 169
ID ADD72505 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 170
ID ADE19378 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 171
ID ADE18826 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 172
ID ADE43022 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 173
ID ADD95811 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 174
ID ADE22697 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 175
ID ADD78815 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 176
ID ADE32765 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 177
ID ADE42457 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match          100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
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RESULT 178
ID ADE17156 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 179
ID ADD80473 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 180
ID ADD89501 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 181
ID ADE40785 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 182
ID ADE04584 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 183
ID ADE92713 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 184
ID ADF47170 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 185
ID ADG21422 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 186
ID ADG33063 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 187
ID ADF97398 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 188
ID ADG80462 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 189
ID ADG52927 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 190
ID ADG60247 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 191
ID ADG79910 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 192
ID ADH55202 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 193
ID ADH5754 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 194
ID ADI61007 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 195
ID ADI63973 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match      100.0%; Score 1694; DB 7; Length 323;
  Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 196
ID ADI64922 standard; protein; 323 AA.
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DE Novel human secreted and transmembrane protein PRO195.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 197
ID ADI63421 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 198
ID ADH81835 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 199
ID ADH81283 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 200
ID ADM82452 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 201
ID ADN15851 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 202
ID ADN16480 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 203
ID ADN15299 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 204
ID ADN14747 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 7; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 205
ID ADC81009 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.

PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 206
ID ADD76457 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 207
ID ADD87821 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 208
ID ADD86225 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 209
ID ADE75673 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 210
ID ADE48664 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 211
ID ADE41258 standard; protein; 323 AA.
DE Human secreted/transmembrane PRO polypeptide #4.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 212
ID ADE23249 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 213
ID ADE23801 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 214
ID ADE24444 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003092111-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 215
ID ADD87269 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 216
ID ADE89135 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 217
ID ADE18274 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 218
ID ADE8583 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 219
ID ADE89765 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 220
ID ADF61405 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.

PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 221
ID ADF40097 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 222
ID ADF45893 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 223
ID ADE94603 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 224
ID ADE91014 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 225
ID ADE95155 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 226
ID ADE93265 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 227
ID ADF24289 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 228
ID ADF40721 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1694; DB 8; Length 323;
RESULT 229
ID ADF23665 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003203402-A1.

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PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 230
ID ADF33648 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 231
ID ADF34846 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 232
ID ADF27115 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 233
ID ADF27751 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 234
ID ADE92161 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 235
ID ADE90462 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 236
ID ADF41345 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 237
ID ADF33024 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 238
ID ADF25390 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 239
ID ADF26491 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 240
ID ADF34280 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 241
ID ADF46517 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 242
ID ADE91609 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 243
ID ADG02188 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 244
ID ADG21974 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 245
ID ADG20044 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 246
ID ADF97950 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 247
ID ADG24167 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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RESULT 266
ID ADG61917 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 267
ID ADG82118 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 268
ID ADG57357 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 269
ID ADG56805 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 270
ID ADG55701 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 271
ID ADG58461 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 272
ID ADG70827 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 273
ID ADG57909 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 274
ID ADG53493 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 275
ID ADG49255 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.

ID ADG71379 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 276
ID ADG50503 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 277
ID ADG81566 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 278
ID ADH30528 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 279
ID ADH11895 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 280
ID ADG49879 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 281
ID ADG51751 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 282
ID ADG52317 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 283
ID ADG54045 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 284
ID ADG49255 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.

PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 285
ID ADG81014 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 286
ID ADG56253 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 287
ID ADH12519 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 288
ID ADG48631 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 289
ID ADG61365 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 290
ID ADH28452 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 291
ID ADG54597 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 292
ID ADG59637 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 293
ID ADG51127 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004005312-A1.

PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 294
ID ADH43441 standard; protein; 323 AA.
DE Human PRO polypeptide #4.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 295
ID ADG59071 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 296
ID ADG62527 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 297
ID ADI81061 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 298
ID ADH25552 standard; protein; 323 AA.
DE Human neurotrophin homologue related protein sequence SEQ ID NO:330.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 299
ID ADG09804 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 300
ID ADI15275 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 301
ID ADG09152 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 302
ID ADI14607 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207383-A1.
PD 06-NOV-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 303
ID ADL18202 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 304
ID ADL13089 standard; protein; 323 AA.
DE Human steroid-induced C3A liver cell protein #128.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 305
ID ADJ63483 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 306
ID ADJ77378 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 307
ID ADK82786 standard; protein; 323 AA.
DE Human PRO polypeptide #4.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 308
ID ADJ65500 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 309
ID ADL13179 standard; protein; 323 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3412.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 310
ID ADM27636 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 311
ID ADM17329 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 312
ID ADI07163 standard; protein; 323 AA.
DE Human secreted/transmembrane protein, PRO195.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 313
ID ADM42360 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 314
ID ADM28222 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 315
ID ADI95704 standard; protein; 323 AA.
DE Human PRO polypeptide #136.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 316
ID ADI96256 standard; protein; 323 AA.
DE Novel human secreted and transmembrane protein PRO195.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 317
ID ADT94201 standard; protein; 323 AA.
DE Human PRO195 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1694; DB 8; Length 323;
Best Local Similarity 100.0%; Pred. No. 8.4e-167;
RESULT 318
ID AAY02282 standard; protein; 324 AA.
DE Secreted protein clone bm41_7 polypeptide sequence.
PN WO9918127-A1.
PD 15-APR-1999.
PA (GEMY ) GENETICS INST INC.
Query Match 98.8%; Score 1674.5; DB 2; Length 324;
Best Local Similarity 99.4%; Pred. No. 8.9e-165;
RESULT 319
ID ADA45143 standard; protein; 324 AA.
DE Human polypeptide #63.
PN US2003044935-A1.
PD 06-MAR-2003.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LVAL/) LA VALLE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAUV) SPAULDING V.
Query Match 98.8%; Score 1674.5; DB 7; Length 324;
Best Local Similarity 99.4%; Pred. No. 8.9e-165;
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RESULT 320
ID ADC37347 standard; protein, 324 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 180.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 98.8%; Score 1674.5; DB 7; Length 324;
Best Local Similarity 99.4%; Pred. No. 8.9e-165;
RESULT 321
ID ADIG2986 standard; protein, 324 AA.
DE Human apoptosis-associated protein SEQ ID 429.
PN WO2003058021-A2.
PD 17-JUL-2003.
PA (XANT-) XANTOS BIOMEDICINE AG.
Query Match 98.8%; Score 1674.5; DB 7; Length 324;
Best Local Similarity 99.4%; Pred. No. 8.9e-165;
RESULT 322
ID ADC37343 standard; protein, 323 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 176.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH) ASAH KASEI KK.
Query Match 95.1%; Score 1611; DB 7; Length 323;
Best Local Similarity 94.1%; Pred. No. 3.5e-158;
RESULT 323
ID AAV17299 standard; protein, 300 AA.
DE Human CBCADB07 polypeptide.
PN WO936522-A1.
PD 22-JUL-1999.
PA (UVSH-) UNIV SHANGHAI SECOND MEDICAL.
Query Match 93.0%; Score 1576; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
RESULT 324
ID ABP71501 standard; protein, 300 AA.
DE Amino acid sequence of protein AAC39890.
PN WO2003006687-A2.
PD 23-JAN-2003.
PA (MEDI-) MEDIGENE AG.
Query Match 93.0%; Score 1576; DB 6; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-154;
RESULT 325
ID ABR43173 standard; protein, 256 AA.
DE Human REMAP-5 protein SEQ ID NO:5.
PN WO2003025130-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 75.8%; Score 1283.5; DB 6; Length 256;
Best Local Similarity 79.3%; Pred. No. 2.6e-124;
RESULT 326
ID AAW74884 standard; protein, 273 AA.
DE Human secreted protein encoded by gene 157 clone HLTED27.
PN WO9839448-A2.
PD 11-SEP-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.5%; Score 1262.5; DB 2; Length 273;
Best Local Similarity 93.5%; Pred. No. 4.3e-122;
RESULT 327
ID ABG95336 standard; protein, 273 AA.
DE Human novel secreted protein #157.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.5%; Score 1262.5; DB 5; Length 273;
Best Local Similarity 93.5%; Pred. No. 4.3e-122;
RESULT 328
ID ABO34530 standard; protein, 273 AA.
DE Region of human secreted protein encoded by cDNA sequence #157.
PN US2003049618-A1.
PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOP/) SOPPET D R.
PA (CART/) CARTER K C.

PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 74.5%; Score 1262.5; DB 6; Length 273;
Best Local Similarity 93.5%; Pred. No. 4.3e-122;
RESULT 329
ID ADI23191 standard; protein, 273 AA.
DE Novel human secreted protein seq id 476.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (LIY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match 74.5%; Score 1262.5; DB 7; Length 273;
Best Local Similarity 93.5%; Pred. No. 4.3e-122;
RESULT 330
ID ADH74193 standard; protein, 273 AA.
DE Human secreted protein #157.
PN US2003225248-A1.
PD 04-DEC-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 74.5%; Score 1262.5; DB 8; Length 273;
Best Local Similarity 93.5%; Pred. No. 4.3e-122;
RESULT 331
ID AAU30578 standard; protein, 345 AA.
DE Novel human secreted protein #1069.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 67.4%; Score 1142; DB 4; Length 345;
Best Local Similarity 76.8%; Pred. No. 1.9e-109;
RESULT 332
ID ADQ65587 standard; protein, 193 AA.

DE Novel human protein sequence #560.
PN EP1440981-A2.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 57.4%; Score 972.5; DB 8; Length 193;
Best Local Similarity 99.0%; Pred. No. 3.4e-92;
RESULT 333
ID ABB04513 standard; protein; 183 AA.
DE Murine apoptosis related protein #1.
PN DE10126344-A1.
PD 24-JAN-2002.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 55.5%; Score 941; DB 5; Length 183;
Best Local Similarity 95.6%; Pred. No. 5.9e-89;
RESULT 334
ID AAG00091 standard; protein; 132 AA.
DE Human secreted protein, SEQ ID NO: 4172.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEBST) GENSET.
Query Match 41.7%; Score 707; DB 3; Length 132;
Best Local Similarity 100.0%; Pred. No. 7.3e-65;
RESULT 335
ID AAY11918 standard; protein; 113 AA.
DE Human 5' EST secreted protein SEQ ID NO: 518.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEBST) GENSET.
Query Match 30.2%; Score 512; DB 2; Length 113;
Best Local Similarity 94.2%; Pred. No. 1e-44;
RESULT 336
ID AAY12407 standard; protein; 88 AA.
DE Human 5' EST secreted protein SEQ ID NO: 438.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEBST) GENSET.
Query Match 26.9%; Score 456; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.8e-39;
RESULT 337
ID AAY16785 standard; protein; 342 AA.
DE Human secreted protein (clone ct489_14).
PN WO9924469-A1.
PD 20-MAY-1999.
PA (GEMV) GENETICS INST INC.
Query Match 25.0%; Score 423.5; DB 2; Length 342;
Best Local Similarity 33.5%; Pred. No. 8e-35;
RESULT 338
ID AAB00163 standard; protein; 342 AA.
DE Brain specific membrane anchored protein (BSMAP).
PN WO200055317-A1.
PD 21-SEP-2000.
PA (FABR) FABRE MEDICAMENT SA PIERRE.
Query Match 25.0%; Score 423.5; DB 3; Length 342;
Best Local Similarity 33.5%; Pred. No. 8e-35;
RESULT 339
ID AAM25782 standard; protein; 353 AA.
DE Human protein sequence SEQ ID NO: 1297.
PN WO200153455-A2.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.0%; Score 423.5; DB 4; Length 353;
Best Local Similarity 33.5%; Pred. No. 8.3e-35;
RESULT 340
ID ADA45175 standard; protein; 342 AA.
DE Human polypeptide #75.
PN US2003044935-A1.
PD 06-MAR-2003.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LVALL/) LA VALLIE E R.
PA (COLL/) COLLINS-RACIB L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.

PA (TREA/) TREACY M.
PA (SPAUV/) SPAULDING V.
Query Match 24.6%; Score 416.5; DB 7; Length 342;
Best Local Similarity 33.0%; Pred. No. 4.2e-34;
RESULT 341
ID ABP69819 standard; protein; 93 AA.
DE Human polypeptide SEQ ID NO 1866.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 19.6%; Score 331.5; DB 5; Length 93;
Best Local Similarity 80.7%; Pred. No. 4.4e-26;
RESULT 342
ID AUA30577 standard; protein; 96 AA.
DE Novel human secreted protein #1068.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 19.6%; Score 331.5; DB 4; Length 96;
Best Local Similarity 80.7%; Pred. No. 4.6e-26;
RESULT 343
ID ADG14985 standard; protein; 286 AA.
DE Human SECP-18 protein.
PN WO2003087300-A2.
PD 23-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 19.2%; Score 324.5; DB 7; Length 286;
Best Local Similarity 32.1%; Pred. No. 1.2e-24;
RESULT 344
ID ADJ66975 standard; protein; 309 AA.
DE Human secreted protein (SECP) #1.
PN WO2004007527-A2.
PD 22-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 18.7%; Score 317.5; DB 8; Length 309;
Best Local Similarity 38.1%; Pred. No. 7e-24;
RESULT 345
ID AAB00167 standard; protein; 251 AA.
DE Brain specific membrane anchored protein (BSMAP) fragment.
PN WO200055317-A1.
PD 21-SEP-2000.
PA (FABR) FABRE MEDICAMENT SA PIERRE.
Query Match 18.6%; Score 314.5; DB 3; Length 251;
Best Local Similarity 33.3%; Pred. No. 1.1e-23;
RESULT 346
ID AAB00166 standard; protein; 114 AA.
DE Brain specific membrane anchored protein (BSMAP) fragment.
PN WO200055317-A1.
PD 21-SEP-2000.
PA (FABR) FABRE MEDICAMENT SA PIERRE.
Query Match 9.9%; Score 168; DB 3; Length 114;
Best Local Similarity 38.7%; Pred. No. 5.6e-09;
RESULT 347
ID AAB00168 standard; protein; 80 AA.
DE Brain specific membrane anchored protein (BSMAP) fragment.
PN WO200055317-A1.
PD 21-SEP-2000.
PA (FABR) FABRE MEDICAMENT SA PIERRE.
Query Match 5.9%; Score 100; DB 3; Length 80;
Best Local Similarity 51.9%; Pred. No. 0.039;
RESULT 348
ID ADH17466 standard; protein; 914 AA.
DE Human NOV13f protein - SEQ ID 156.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 99; DB 8; Length 914;
Best Local Similarity 19.7%; Pred. No. 1.6;
RESULT 349
ID ABP62957 standard; protein; 811 AA.
DE Human polypeptide SEQ ID NO 394.
PN WO200218424-A2.
PD 07-MAR-2002.

PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 96; DB 5; Length 811;
Best Local Similarity 19.4%; Pred. No. 2.8;
RESULT 350
ID ABL10550 standard; protein; 896 AA.
DE Human NOV4b protein.
PN WO200246408-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 96; DB 5; Length 896;
Best Local Similarity 19.4%; Pred. No. 3.3;
RESULT 351
ID ADH17468 standard; protein; 896 AA.
DE Human NOV13g protein - SEQ ID 158.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 96; DB 8; Length 896;
Best Local Similarity 19.4%; Pred. No. 3.3;
RESULT 352
ID ADH17468 standard; protein; 920 AA.
DE Human NOV14i protein - SEQ ID 178.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 96; DB 8; Length 920;
Best Local Similarity 19.4%; Pred. No. 3.4;
RESULT 353
ID ADQ59436 standard; protein; 922 AA.
DE Human cancer-associated (CA) protein sequence SEQ ID NO:72.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.7%; Score 96; DB 8; Length 922;
Best Local Similarity 19.4%; Pred. No. 3.4;
RESULT 354
ID ADH17464 standard; protein; 945 AA.
DE Human NOV13e protein - SEQ ID 154.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 96; DB 8; Length 945;
Best Local Similarity 19.4%; Pred. No. 3.5;
RESULT 355
ID AAB38627 standard; protein; 471 AA.
DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:164.
PN WO200056882-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 95.5; DB 3; Length 471;
Best Local Similarity 18.0%; Pred. No. 1.5;
RESULT 356
ID ADR41504 standard; protein; 486 AA.
DE Human CD-1 like molecule HMBFK1, SEQ ID NO:303.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 95.5; DB 5; Length 486;
Best Local Similarity 18.0%; Pred. No. 1.5;
RESULT 357
ID AAB95417 standard; protein; 537 AA.
DE Human protein sequence SEQ ID NO:17814.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.6%; Score 95.5; DB 4; Length 537;
Best Local Similarity 18.0%; Pred. No. 1.8;
RESULT 358
ID ADU69381 standard; protein; 741 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1187.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
Query Match 5.6%; Score 95.5; DB 7; Length 741;
Best Local Similarity 18.0%; Pred. No. 2.8;
RESULT 359
ID ADQ21134 standard; protein; 741 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3954.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.6%; Score 95.5; DB 8; Length 741;
Best Local Similarity 18.0%; Pred. No. 2.8;
RESULT 360
ID ABP62956 standard; protein; 830 AA.
DE Human polypeptide SEQ ID NO 393.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 95.5; DB 5; Length 830;
Best Local Similarity 18.0%; Pred. No. 3.3;
RESULT 361
ID AAY13350 standard; protein; 915 AA.
DE Amino acid sequence of protein PRO219.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 2; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 362
ID AAY95340 standard; protein; 915 AA.
DE Human PRO219 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH-) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 3; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 363
ID ADC78354 standard; protein; 915 AA.
DE Human PRO219 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 3; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 364
ID AAB80218 standard; protein; 915 AA.
DE Human PRO219 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 365
ID AAU12318 standard; protein; 915 AA.
DE Human PRO219 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH-) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 366
ID AAB53077 standard; protein; 915 AA.
DE Human angiogenesis-associated protein PRO219, SEQ ID NO:67.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH-) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 4; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 367
ID ABU71596 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH-) GENENTECH INC.

Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 368
ID ABO17762 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 369
ID ABU71451 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 370
ID ABU81016 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 371
ID ABU71897 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 372
ID ABO01780 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 373
ID ABU66716 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 374
ID ABU54353 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US200213240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 375
ID ABO47368 standard; protein; 915 AA.
DE Human secreted/transmembrane polypeptide PRO219.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 376
ID ABU59797 standard; protein; 915 AA.
DE Novel secreted and transmembrane protein PRO219.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 377
ID ABO24987 standard; protein; 915 AA.
DE Human secreted/transmembrane protein (PRO) #147.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 378
ID ABU64505 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 379
ID ABU67351 standard; protein; 915 AA.
DE Human secreted protein PRO219.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 380
ID ABO14871 standard; protein; 915 AA.
DE Human secreted / transmembrane polypeptide PRO219.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 381
ID ABU66992 standard; protein; 915 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 294.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 382
ID ABU69628 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 383
ID ABO14810 standard; protein; 915 AA.
DE Human secreted / transmembrane polypeptide PRO219.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 384
ID ADA45813 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 385
ID ADA76244 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;

RESULT 386
ID ADB29239 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 387
ID ADA18894 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 388
ID ADA61517 standard; protein; 915 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 389
ID ADB19302 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 390
ID ADB27843 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 391
ID ADA86322 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 392
ID ADB15886 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 393
ID ADA47672 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 394
ID ADA18095 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 395

ID ABO32762 standard; protein; 915 AA.
DE Human secreted/transmembrane protein PRO219.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 396
ID ADA67467 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 397
ID ADB30474 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 398
ID ADA85770 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 399
ID ADA96982 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 400
ID ADA79286 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 401
ID ADA87425 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 402
ID ADB16627 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 403
ID ABO34822 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 404
ID ADA16070 standard; protein; 915 AA.

DE Human secreted/transmembrane protein, #8.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 405
ID ADA91719 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 406
ID ADB14782 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 407
ID ADB18743 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 408
ID ADA93958 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 409
ID ADB19854 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 410
ID ADB13166 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 411
ID ABO43295 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 412
ID ADA74420 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 413
ID ADA42215 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.

PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 414
ID ADB24653 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 415
ID ADA82177 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 416
ID ADA75140 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 417
ID ADA85218 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 418
ID ADA84666 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 419
ID ABO17500 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 420
ID ADB29922 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 421
ID ADA80450 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 422
ID ADA75692 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082703-A1.

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PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 423
ID ADA46917 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 424
ID ADB25213 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 425
ID ADA93389 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 426
ID ADB26739 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 427
ID ADB31026 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 428
ID ADA60954 standard; protein; 915 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 429
ID ADB24101 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 430
ID ADA96430 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 431
ID ADA81002 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 432
ID ADA95878 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 433
ID ADB26187 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 434
ID ADB21672 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 6; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 435
ID ADA77451 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 436
ID ADB18191 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 437
ID ADA66874 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 438
ID ADA16494 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 439
ID ADA12923 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 440
ID ADA41791 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 441
ID ADA87977 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 442
ID ADA46365 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 443
ID ADA17138 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 444
ID ADA42641 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 445
ID ADB28395 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 446
ID ADB28947 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 447
ID ADA76899 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 448
ID ADA86529 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 449
ID ADA97534 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 450
ID ADB27291 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 451
ID ADB22224 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 452
ID ABO17561 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 453
ID ADA66915 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 454
ID ADB22776 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 455
ID ADB23549 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 456
ID ADA92271 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 457
ID ADB15334 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 458
ID ADB38586 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 459
ID ADB38034 standard; protein; 915 AA.

DE Novel human secreted and transmembrane protein PRO219.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 460
ID ADB6506 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 461
ID ADB89586 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 462
ID ADB90318 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 463
ID ADB77560 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 464
ID ADB39419 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 465
ID ADB74696 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 466
ID ADB47042 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 467
ID ADB86649 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 468
ID ADB77254 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.

PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 469
ID ADB34411 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 470
ID ADB35515 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 471
ID ADB33859 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 472
ID ADB34963 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 473
ID ADB36067 standard; protein; 915 AA.
DE Human PRO polypeptide SEQ ID NO 294.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 474
ID ADB46462 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 475
ID ADC28342 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 476
ID ADC39542 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 477
ID ADC40056 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003059829-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 478
ID ADC18884 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 479
ID ADC34180 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 480
ID ADC29235 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 481
ID ADC28766 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 482
ID ADC40651 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 483
ID ADC19308 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 484
ID ADC33756 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 485
ID ADC12826 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 486
ID ADC50335 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092106-A1.
PD 15-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 487
ID ADC71882 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 488
ID ADC59861 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 489
ID ADC52868 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 490
ID ADC57222 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 491
ID ADC60413 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 492
ID ADC50888 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 493
ID ADC65415 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 494
ID ADC54513 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 495
ID ADC53474 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 496
ID ADC58997 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 497
ID ADC55875 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 498
ID ADC58445 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein Seq ID294.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 499
ID ADC12278 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 500
ID ADD03119 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 501
ID ADC90111 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 502
ID ADC69530 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 503
ID ADC48419 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 504
ID ADD09948 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 505
ID ADD03415 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 505
ID ADD04523 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 506
ID ADC80479 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 507
ID ADD10986 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 508
ID ADC47867 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 509
ID ADD04833 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 510
ID ADC79927 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 511
ID ADD09396 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 512
ID ADD03839 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 513
ID ADD03415 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;

RESULT 514
ID ADD41109 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 515
ID ADD52248 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 516
ID ADD52988 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 517
ID ADD53540 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 518
ID ADD51696 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 519
ID ADD02495 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 520
ID ADD01929 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 521
ID ADD54111 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 522
ID ADD92428 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 523

ID ADD91324 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 524
ID ADE03938 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 525
ID ADE32235 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 526
ID ADE32167 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 527
ID ADD79391 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 528
ID ADE41927 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 529
ID ADE17744 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 530
ID ADD91876 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 531
ID ADE33339 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 532
ID ADE33891 standard; protein; 915 AA.


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DE Novel human secreted and transmembrane protein PRO219.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 533
ID ADD79943 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 534
ID ADD92980 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 535
ID ADE19400 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 536
ID ADE34667 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 537
ID ADE18848 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 538
ID ADE43044 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 539
ID ADD95833 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 540
ID ADE32719 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 541
ID ADD78837 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207384-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 542
ID ADE32787 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 543
ID ADE42479 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 544
ID ADD80495 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 545
ID ADD89523 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 546
ID ADE40807 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 547
ID ADE04606 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 548
ID ADE92735 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 549
ID ADG21444 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 550
ID ADG23085 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207384-A1.
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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 551
ID ADP97420 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 552
ID ADG80484 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 553
ID ADG79932 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 554
ID ADH59150 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 555
ID ADH55224 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 556
ID ADH55776 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 557
ID ADI37929 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 558
ID ADI63995 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 559
ID ADI64944 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207386-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 560
ID ADI63443 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 561
ID ADH81857 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 562
ID ADH81305 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 563
ID ADJ26197 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 564
ID ADM82474 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 565
ID ADN15673 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 566
ID ADN16502 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 567
ID ADN15321 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 568
ID ADN14769 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 5.6%; Score 95.5; DB 7; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 569
ID ADC81031 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 570
ID ADE79112 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 571
ID ADD76479 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 572
ID ADD87843 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 573
ID ADE86247 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 574
ID ADE79536 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 575
ID ADE75695 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 576
ID ADE73212 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 577
ID ADE3271 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 578
ID ADE23823 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 579
ID ADE24466 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 580
ID ADD87291 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 581
ID ADE89157 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 582
ID ADE73747 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 583
ID ADE18296 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 584
ID ADE88605 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 585
ID ADE99301 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 586
ID ADE94625 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;

RESULT 587
ID ADE91036 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 588
ID ADE95177 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 589
ID ADE93287 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 590
ID ADF34868 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 591
ID ADE98420 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 592
ID ADE92183 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 593
ID ADE90484 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 594
ID ADE91631 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 595
ID ADE98847 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 596

ID ADG40317 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 597
ID ADF73711 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 598
ID ADG02210 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 599
ID ADG21996 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 600
ID ADG20066 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 601
ID ADF97972 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 602
ID ADG24189 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 603
ID ADF98543 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 604
ID ADG03374 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207351-A1.


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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 605
ID ADF99095 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 606
ID ADG16680 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 607
ID ADG05139 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 608
ID ADG19406 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 609
ID ADF73287 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 610
ID ADG13243 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 611
ID ADG08300 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 612
ID ADG15470 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 613
ID ADF96868 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 614
ID ADG06053 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 615
ID ADG23637 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 616
ID ADG03926 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 617
ID ADG24827 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 618
ID ADG07124 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 619
ID ADG07676 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 620
ID ADG55171 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 621
ID ADG60835 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 622
ID ADG61939 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
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Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 623
ID ADG92130 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 624
ID ADG82140 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 625
ID ADG57379 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 626
ID ADG56827 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 627
ID ADG55723 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 628
ID ADG58483 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 629
ID ADG70849 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 630
ID ADG92557 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 631
ID ADG57931 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;

Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 632
ID ADG53515 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 633
ID ADG71401 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 634
ID ADG81588 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 635
ID ADH30550 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 636
ID ADH11917 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 637
ID ADG52339 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 638
ID ADG54067 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 639
ID ADG81036 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 640
ID ADG56275 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 641

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ID ADH12541 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 642
ID ADG61387 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 643
ID ADH28474 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 644
ID ADG54619 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 645
ID ADG59659 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 646
ID ADH20346 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 647
ID ADH07201 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 648
ID ADH59746 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 649
ID ADH06774 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 650
ID ADI1083 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 651
ID ADI18516 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 652
ID ADI65236 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 653
ID ADI37499 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 654
ID ADG09826 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 655
ID ADH97303 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 656
ID ADI15297 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 657
ID ADG09174 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match      5.6%; Score 95.5; DB 8; Length 915;
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Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 658
ID ADI65663 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 659
ID ADI14629 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 660
ID ADH60406 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 661
ID ADI18224 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 662
ID ADJ99463 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 663
ID ADL08656 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 664
ID ADM25001 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 665
ID ADJ63505 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 666
ID ADM29747 standard; protein; 915 AA.

DE Human secreted/transmembrane protein, #8.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 667
ID ADJ77400 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 668
ID ADJ65522 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 669
ID ADM27658 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 670
ID ADM42382 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 671
ID ADO06069 standard; protein; 915 AA.
DE Human PRO polypeptide #7.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 672
ID ADM28244 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 673
ID ADR10921 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 5.6%; Score 95.5; DB 8; Length 915;
Best Local Similarity 18.0%; Pred. No. 3.8;
RESULT 674
ID ADR17830 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.

PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 675
ID ADI95726 standard; protein; 915 AA.
DE Human PRO polypeptide #147.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 676
ID ADI96278 standard; protein; 915 AA.
DE Novel human secreted and transmembrane protein PRO219.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 677
ID ADT03506 standard; protein; 915 AA.
DE Human secreted/transmembrane protein, #8.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 678
ID ADS74469 standard; protein; 915 AA.
DE Human secreted/transmembrane protein #8.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANU/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.

Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 915;
Pred. No. 3.8;
RESULT 679
ID AAB03843 standard; protein; 934 AA.
DE Human gene 3 encoded secreted protein HOGDPA6, SEQ ID NO: 89.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 4; Length 934;
Pred. No. 3.9;
RESULT 680
ID ABG64542 standard; protein; 934 AA.
DE Human albumin fusion protein #1217.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 5; Length 934;
Pred. No. 3.9;
RESULT 681
ID ADL77809 standard; protein; 934 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1291.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 934;
Pred. No. 3.9;
RESULT 682
ID ADH17484 standard; protein; 939 AA.
DE Human NOV14g protein - SEQ ID 174.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 939;
Pred. No. 3.9;
RESULT 683
ID ADH17462 standard; protein; 964 AA.
DE Human NOV13d protein - SEQ ID 152.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 964;
Pred. No. 4.1;
RESULT 684
ID ADH17460 standard; protein; 964 AA.
DE Human NOV13c protein - SEQ ID 150.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 8; Length 964;
Pred. No. 4.1;
RESULT 685
ID AAE03877 standard; protein; 983 AA.
DE Human gene 3 encoded secreted protein fragment, SEQ ID NO:127.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.6%; Score 95.5; DB 4; Length 983;
Pred. No. 4.2;
RESULT 686
ID AAY37126 standard; protein; 388 AA.
DE Protein involved in intermediate metabolism of sugars and/or cofactors.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 5.6%; Score 94.5; DB 2; Length 388;
Pred. No. 1.4;
RESULT 687
ID ADJ70087 standard; protein; 956 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqId1893.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
Query Match 5.5%; Score 93.5; DB 7; Length 956;
Best Local Similarity 18.0%; Pred. No. 6.5;
RESULT 688
ID ADM12924 standard; protein; 956 AA.
DE PRO83470 protein.
PN WO2004024077-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 93.5; DB 8; Length 956;
Best Local Similarity 18.0%; Pred. No. 6.5;
RESULT 689
ID ADN03855 standard; protein; 956 AA.
DE Antipsoriatic protein sequence #123.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.5%; Score 93.5; DB 8; Length 956;
Best Local Similarity 18.0%; Pred. No. 6.5;
RESULT 690
ID AAB20159 standard; protein; 959 AA.
DE Human protein SECP5.
PN WO200105971-A2.
PD 25-JAN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 92; DB 4; Length 959;
Best Local Similarity 17.9%; Pred. No. 9.4;
RESULT 691
ID ADG38840 standard; protein; 959 AA.
DE Human SECP5.
PN US2003207348-A1.
PD 06-NOV-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E R.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (GUSE/) GUSEV V Y.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
Query Match 5.4%; Score 92; DB 7; Length 959;
Best Local Similarity 17.9%; Pred. No. 9.4;
RESULT 692
ID ADH17470 standard; protein; 959 AA.
DE Human NOV13h protein - SEQ ID 160.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 92; DB 8; Length 959;
Best Local Similarity 17.9%; Pred. No. 9.4;
RESULT 693
ID ADH17456 standard; protein; 959 AA.
DE Human NOV13a protein - SEQ ID 146.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 92; DB 8; Length 959;
Best Local Similarity 17.9%; Pred. No. 9.4;
RESULT 694
ID ABJ10549 standard; protein; 977 AA.
DE Human NOV4a protein.
PN WO200246408-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.4%; Score 92; DB 5; Length 977;
Best Local Similarity 17.9%; Pred. No. 9.6;
RESULT 695
ID ABB94365 standard; protein; 527 AA.
DE Chlamydia trachomatis protein sequence SEQ ID NO:588.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.

Query Match 5.2%; Score 88.5; DB 5; Length 527;
Best Local Similarity 19.5%; Pred. No. 9.2;
RESULT 696
ID AAE03820 standard; protein; 794 AA.
DE Human gene 3 encoded secreted protein HOGDP46, SEQ ID NO: 66.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 88.5; DB 4; Length 794;
Best Local Similarity 18.8%; Pred. No. 17;
RESULT 697
ID ABG64543 standard; protein; 794 AA.
DE Human albumin fusion protein #1218.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.2%; Score 88.5; DB 5; Length 794;
Best Local Similarity 18.8%; Pred. No. 17;
RESULT 698
ID ADL77810 standard; protein; 794 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1292.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 5.2%; Score 88.5; DB 8; Length 794;
Best Local Similarity 18.8%; Pred. No. 17;
RESULT 699
ID ABB62620 standard; protein; 1349 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14652.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 88; DB 4; Length 1349;
Best Local Similarity 22.8%; Pred. No. 40;
RESULT 700
ID ADH17486 standard; protein; 782 AA.
DE Human NOV14h protein - SEQ ID 176.
PN WO2003093432-A2.
PD 13-NOV-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.2%; Score 87.5; DB 8; Length 782;
Best Local Similarity 19.0%; Pred. No. 21;
RESULT 701
ID AAB20158 standard; protein; 776 AA.
DE Human protein SECP4.
PN WO200105971-A2.
PD 25-JAN-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 87; DB 4; Length 776;
Best Local Similarity 18.6%; Pred. No. 23;
RESULT 702
ID ADG38838 standard; protein; 776 AA.
DE Human SECP4.
PN US2003207348-A1.
PD 06-NOV-2003.
PA (SHIM/) SHIMKETS R A.
PA (FERN/) FERNANDES E R.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (GUSE/) GUSEV V Y.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
Query Match 5.1%; Score 87; DB 7; Length 776;
Best Local Similarity 18.6%; Pred. No. 23;
RESULT 703
ID ABJ37049 standard; protein; 997 AA.
DE Human breast cancer / ovarian cancer related protein #25.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 5.1%; Score 86.5; DB 6; Length 997;
Best Local Similarity 24.6%; Pred. No. 37;
RESULT 704
ID ADS26422 standard; protein; 376 AA.
DE Bacterial polypeptide #15455.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 86; DB 8; Length 376;
Best Local Similarity 19.5%; Pred. No. 10;
RESULT 705
ID ADS27172 standard; protein; 386 AA.
DE Bacterial polypeptide #16205.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 86; DB 8; Length 386;
Best Local Similarity 19.5%; Pred. No. 11;
RESULT 706
ID ADS26790 standard; protein; 386 AA.
DE Bacterial polypeptide #15823.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 86; DB 8; Length 386;
Best Local Similarity 19.5%; Pred. No. 11;
RESULT 707
ID ABM83038 standard; protein; 848 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3287.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.1%; Score 86; DB 8; Length 848;
Best Local Similarity 20.8%; Pred. No. 33;
RESULT 708
ID AAM42001 standard; protein; 376 AA.
DE Human polypeptide SEQ ID NO 6932.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 85.5; DB 4; Length 376;
Best Local Similarity 19.8%; Pred. No. 12;
RESULT 709
ID AAO24548 standard; protein; 397 AA.
DE Human BHD mutant truncated protein SEQ ID NO: 6.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.0%; Score 85.5; DB 8; Length 397;
Best Local Similarity 19.8%; Pred. No. 12;
RESULT 710
ID ABM67558 standard; protein; 399 AA.
DE Photorhabdus luminescens protein sequence #655.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.0%; Score 85.5; DB 6; Length 399;
Best Local Similarity 23.0%; Pred. No. 13;
RESULT 711
ID AAO24549 standard; protein; 454 AA.

DE Human BHD mutant truncated protein SEQ ID NO: 8.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.0%; Score 85.5; DB 8; Length 454;
Best Local Similarity 19.8%; Pred. No. 15;
RESULT 712
ID AAO24551 standard; protein; 462 AA.
DE Human BHD mutant truncated protein SEQ ID NO: 12.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.0%; Score 85.5; DB 8; Length 462;
Best Local Similarity 19.8%; Pred. No. 16;
RESULT 713
ID AAO24550 standard; protein; 466 AA.
DE Human BHD mutant truncated protein SEQ ID NO: 10.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.0%; Score 85.5; DB 8; Length 466;
Best Local Similarity 19.8%; Pred. No. 16;
RESULT 714
ID AAO24546 standard; protein; 579 AA.
DE Human BHD protein, folliculin.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.0%; Score 85.5; DB 8; Length 579;
Best Local Similarity 19.8%; Pred. No. 21;
RESULT 715
ID ABP75839 standard; protein; 594 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1023.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.0%; Score 85.5; DB 6; Length 594;
Best Local Similarity 19.8%; Pred. No. 22;
RESULT 716
ID ADJ68448 standard; protein; 3225 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID254.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.0%; Score 85.5; DB 7; Length 3225;
Best Local Similarity 22.2%; Pred. No. 2.5e+02;
RESULT 717
ID ADE56037 standard; protein; 3259 AA.
DE Human Protein CAA53052, SEQ ID NO 1876.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.0%; Score 85.5; DB 7; Length 3259;
Best Local Similarity 22.2%; Pred. No. 2.6e+02;
RESULT 718
ID ADE56033 standard; protein; 3259 AA.
DE Human Protein CAA53052, SEQ ID NO 1872.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.0%; Score 85.5; DB 7; Length 3259;
Best Local Similarity 22.2%; Pred. No. 2.6e+02;
RESULT 719
ID ADP29881 standard; protein; 1096 AA.
DE Human secreted protein SEQ ID #648.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 5.0%; Score 85; DB 8; Length 1096;
Best Local Similarity 19.7%; Pred. No. 61;

RESULT 720
ID AAB95304 standard; protein; 890 AA.
DE Human protein sequence SEQ ID NO:17542.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.0%; Score 84.5; DB 4; Length 890;
Best Local Similarity 18.8%; Pred. No. 51;
RESULT 721
ID ABR82250 standard; protein; 1033 AA.
DE Human nucleic acid-associated protein (NAAP)-Id 1797985CD1.
PN WO2003052048-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.0%; Score 84.5; DB 6; Length 1033;
Best Local Similarity 18.8%; Pred. No. 63;
RESULT 722
ID ABR64202 standard; protein; 1194 AA.
DE Angiogenesis protein BNO381.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match 5.0%; Score 84.5; DB 6; Length 1194;
Best Local Similarity 18.8%; Pred. No. 77;
RESULT 723
ID ADQ66046 standard; protein; 1375 AA.
DE Novel human protein sequence #1019.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.0%; Score 84.5; DB 8; Length 1375;
Best Local Similarity 18.8%; Pred. No. 95;
RESULT 724
ID AAR91296 standard; protein; 1350 AA.
DE Drosophila nitric oxide synthase.
PN WO9611270-A1.
PD 18-APR-1996.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 5.0%; Score 84; DB 2; Length 1350;
Best Local Similarity 22.6%; Pred. No. 1e+02;
RESULT 725
ID ADJ95084 standard; protein; 4313 AA.
DE Novel NOVX protein sequence #156.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.0%; Score 84; DB 7; Length 4313;
Best Local Similarity 22.4%; Pred. No. 5.5e+02;
RESULT 726
ID ADA55192 standard; protein; 376 AA.
DE Human protein, SEQ ID 2760.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.9%; Score 83.5; DB 6; Length 376;
Best Local Similarity 22.5%; Pred. No. 19;
RESULT 727
ID ADQ66652 standard; protein; 623 AA.
DE Novel human protein sequence #1625.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.9%; Score 83.5; DB 8; Length 623;
Best Local Similarity 22.5%; Pred. No. 39;
RESULT 728
ID ABB77985 standard; protein; 1318 AA.
DE Amino acid sequence of a human RAD50 homologue.
PN EP1217074-A1.
PD 26-JUN-2002.
PA (UYLE-) RIJKSUNIV LEIDEN.
PA (BINA-) STICHTING BINAIR VECTOR SYSTEEM.
Query Match 4.9%; Score 83.5; DB 5; Length 1318;

Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 729
ID ADJ68860 standard; protein; 1318 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID666.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.9%; Score 83.5; DB 7; Length 1318;
Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 730
ID ADJ66509 standard; protein; 1318 AA.
DE RAD50 homolog HSRAD50 for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZOME AG.
Query Match 4.9%; Score 83.5; DB 8; Length 1318;
Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 731
ID ADS88326 standard; protein; 1318 AA.
DE Human protein of a TNF-alpha signalling pathway protein complex Seq 181.
PN WO2004035783-A2.
PD 29-APR-2004.
PA (CELL-) CELLZOME AG.
Query Match 4.9%; Score 83.5; DB 8; Length 1318;
Best Local Similarity 23.1%; Pred. No. 1.1e+02;
RESULT 732
ID ABG14228 standard; protein; 1664 AA.
DE Novel human diagnostic protein #14219.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 83.5; DB 4; Length 1664;
Best Local Similarity 19.7%; Pred. No. 1.6e+02;
RESULT 733
ID AAU29705 standard; protein; 191 AA.
DE Novel human secreted protein #196.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.9%; Score 83; DB 4; Length 191;
Best Local Similarity 29.8%; Pred. No. 7.9;
RESULT 734
ID ABB90643 standard; protein; 500 AA.
DE Chlamydia pneumoniae cp6526 protein, SEQ ID NO:235.
PN WO200202606-A2.
PD 10-JAN-2002.
PA (CHIR-) CHIRON SPA.
Query Match 4.9%; Score 83; DB 5; Length 500;
Best Local Similarity 22.3%; Pred. No. 32;
RESULT 735
ID AAY34845 standard; protein; 503 AA.
DE Chlamydia pneumoniae transmembrane protein sequence.
PN WO9927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 4.9%; Score 83; DB 2; Length 503;
Best Local Similarity 22.3%; Pred. No. 32;
RESULT 736
ID ABU26912 standard; protein; 503 AA.
DE Protein encoded by Prokaryotic essential gene #12439.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 83; DB 6; Length 503;
Best Local Similarity 22.3%; Pred. No. 32;
RESULT 737
ID AAW50897 standard; protein; 1607 AA.
DE Mouse laminin G1 chain.
PN WO9815179-A1.
PD 16-APR-1998.
PA (UNIW) UNIV WASHINGTON.
Query Match 4.9%; Score 83; DB 2; Length 1607;


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Best Local Similarity 22.8%; Pred. No. 1.7e+02;
RESULT 738
ID ABB6371 standard; protein; 415 AA.
DE Novel human diagnostic protein #26362.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 19.3%; Pred. No. 27; Length 415;
RESULT 739
ID AAO24552 standard; protein; 579 AA.
DE Murine BHD protein.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 19.4%; Pred. No. 44; Length 579;
RESULT 740
ID ADC96058 standard; protein; 698 AA.
DE E. faecium protein sequence SEQ ID 5685.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENC-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 20.2%; Pred. No. 58; Length 698;
RESULT 741
ID ABB96081 standard; protein; 769 AA.
DE Human protein kinase SEQ ID NO:68.
PN WO200300901-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match
Best Local Similarity 4.9%; Score 82.5; DB 6; Length 769;
RESULT 742
ID ABB57101 standard; protein; 859 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:228.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match
Best Local Similarity 4.9%; Score 82.5; DB 5; Length 859;
RESULT 743
ID ADE54207 standard; protein; 859 AA.
DE Rat Protein NP 038587, SEQ ID NO 10.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match
Best Local Similarity 4.9%; Score 82.5; DB 7; Length 859;
RESULT 744
ID ADE54203 standard; protein; 859 AA.
DE Rat Protein NP 038587, SEQ ID NO 6.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match
Best Local Similarity 4.9%; Score 82.5; DB 7; Length 859;
RESULT 745
ID AAP91380 standard; peptide; 119 AA.
DE Porcine prepromotilin.
PN WO8907611-A.
PD 24-AUG-1989.
PA (UYOR-) OREGON UNIVERSITY.
Query Match
Best Local Similarity 4.8%; Score 82; DB 1; Length 119;
RESULT 746
ID AAB20102 standard; protein; 119 AA.
DE Pig motilin.
PN WO200100830-A1.
PD 04-JAN-2001.
PA (ZYMO-) ZYMOGENETICS INC.

Query Match
Best Local Similarity 4.8%; Score 82; DB 4; Length 119;
RESULT 747
ID AAB62651 standard; protein; 119 AA.
DE Motilin receptor, GPR38.
PN WO200138355-A2.
PD 31-MAY-2001.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match
Best Local Similarity 4.8%; Score 82; DB 4; Length 119;
RESULT 748
ID ADI33329 standard; protein; 119 AA.
DE Pig motilin protein homologous to Zsig33.
PN US2003176640-A1.
PD 18-SEP-2003.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match
Best Local Similarity 4.8%; Score 82; DB 7; Length 119;
RESULT 749
ID ADN11759 standard; protein; 119 AA.
DE Porcine motilin protein.
PN WO2004033645-A2.
PD 22-APR-2004.
PA (ZYMO-) ZYMOGENETICS INC.
Query Match
Best Local Similarity 4.8%; Score 82; DB 8; Length 119;
RESULT 750
ID ABB55253 standard; protein; 307 AA.
DE Lactococcus lactis protein cfa.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 4.8%; Score 82; DB 5; Length 307;
RESULT 751
ID AAB93590 standard; protein; 520 AA.
DE Human protein sequence SEQ ID NO:13016.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 4.8%; Score 82; DB 4; Length 520;
RESULT 752
ID AAB94160 standard; protein; 557 AA.
DE Human protein sequence SEQ ID NO:14452.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 4.8%; Score 82; DB 4; Length 557;
RESULT 753
ID AAB94603 standard; protein; 678 AA.
DE Human protein sequence SEQ ID NO:15428.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 4.8%; Score 82; DB 4; Length 678;
RESULT 754
ID AAB65969 standard; protein; 754 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 109.
PN WO200077023-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.8%; Score 82; DB 4; Length 754;
RESULT 755
ID AAU31665 standard; protein; 1030 AA.
DE Novel human secreted protein #2156.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.

Query Match
Best Local Similarity 20.0%; Pred. No. 73; Length 754;
RESULT 756
ID AAB20102 standard; protein; 119 AA.
DE Pig motilin.
PN WO200100830-A1.
PD 04-JAN-2001.
PA (ZYMO-) ZYMOGENETICS INC.
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Best Local Similarity 20.0%; Pred. No. 1.1e+02;
RESULT 756
ID ADJ70612 standard; protein; 1313 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2418.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.8%; Score 82; DB 7; Length 1313;
Best Local Similarity 18.0%; Pred. No. 1.6e+02;
RESULT 757
ID ABM83605 standard; protein; 1538 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3854.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.8%; Score 82; DB 8; Length 1538;
Best Local Similarity 22.1%; Pred. No. 2e+02;
RESULT 758
ID ADL12580 standard; protein; 1564 AA.
DE Human steroid-induced C3A liver cell protein #44.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.8%; Score 82; DB 8; Length 1564;
Best Local Similarity 20.0%; Pred. No. 2.1e+02;
RESULT 759
ID AAB19801 standard; protein; 1609 AA.
DE Human laminin 2 gamma-1 chain.
PN WO200066730-A2.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 4.8%; Score 82; DB 3; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 760
ID AAB48452 standard; protein; 1609 AA.
DE Human laminin 8 polypeptide, SEQ ID NO: 22.
PN WO200066732-A2.
PD 09-NOV-2000.
PA (BIOS-) BIOSSTRATUM INC.
Query Match 4.8%; Score 82; DB 3; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 761
ID ABB81594 standard; protein; 1609 AA.
DE Human laminin 10 third chain protein sequence SEQ ID NO:14.
PN WO200250111-A2.
PD 27-JUN-2002.
PA (BIOS-) BIOSSTRATUM INC.
Query Match 4.8%; Score 82; DB 5; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 762
ID ADC01887 standard; protein; 1609 AA.
DE Human laminin gamma 1subunit.
PN US2003103975-A1.
PD 05-JUN-2003.
PA (JONE/) JONES J C R.
PA (GONZ/) GONZALES M.
Query Match 4.8%; Score 82; DB 7; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 763
ID ADG37229 standard; protein; 1609 AA.
DE Human laminin-6 B2 subunit.
PN JP2003212791-A.
PD 30-JUL-2003.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 4.8%; Score 82; DB 7; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 764
ID ADP23021 standard; protein; 1609 AA.
DE PRO polypeptide SEQ ID NO:115.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match 4.8%; Score 82; DB 8; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 765
ID AAB19803 standard; protein; 1617 AA.
DE Human laminin 2 gamma-1 chain with C-terminal FLAG epitope.
PN WO200066730-A2.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 4.8%; Score 82; DB 3; Length 1617;
Best Local Similarity 22.1%; Pred. No. 2.2e+02;
RESULT 766
ID ADC06797 standard; protein; 2146 AA.
DE Human prostate cancer-related protein NM_015384.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 4.8%; Score 82; DB 7; Length 2146;
Best Local Similarity 18.0%; Pred. No. 3.3e+02;
RESULT 767
ID ADC06798 standard; protein; 2265 AA.
DE Human prostate cancer-related protein NM_133433.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 4.8%; Score 82; DB 7; Length 2265;
Best Local Similarity 18.0%; Pred. No. 3.5e+02;
RESULT 768
ID ADJ68818 standard; protein; 2265 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID624.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.8%; Score 82; DB 7; Length 2265;
Best Local Similarity 18.0%; Pred. No. 3.5e+02;
RESULT 769
ID ADP24677 standard; protein; 2265 AA.
DE PRO polypeptide SEQ ID NO:1855.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 82; DB 8; Length 2265;
Best Local Similarity 18.0%; Pred. No. 3.5e+02;
RESULT 770
ID ADC06796 standard; protein; 2685 AA.
DE Human prostate cancer-related protein PCP0623.
PN WO2003064599-A2.
PD 07-AUG-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 4.8%; Score 82; DB 7; Length 2685;
Best Local Similarity 18.0%; Pred. No. 4.5e+02;
RESULT 771
ID ADN04576 standard; protein; 2804 AA.
DE Antipneumatic protein sequence #477.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.8%; Score 82; DB 8; Length 2804;
Best Local Similarity 18.0%; Pred. No. 4.8e+02;
RESULT 772
ID AAW62831 standard; protein; 525 AA.
DE Theobroma cacao antimicrobial protein.
PN WO9827805-A1.
PD 02-JUL-1998.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
Query Match 4.8%; Score 81.5; DB 2; Length 525;
Best Local Similarity 22.6%; Pred. No. 49;
RESULT 773
ID AAR20181 standard; protein; 566 AA.
DE Sequence encoded by 67 kD T. cacao protein cDNA.
PN WO9119801-A.
PD 26-DEC-1991.
PA (MRSC) MARS UK LTD.

Query Match 4.8%; Score 81.5; DB 2; Length 566;
Best Local Similarity 22.6%; Pred. No. 54;
RESULT 774
ID ADI40495 standard; protein; 567 AA.
DE Human purified secretory polypeptide (SPTM), seq id 188.
PN WO2003062385-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (JONE-) JONES A L.
PA (DAHL-) DAHL C R.
PA (GIET-) GIETZEN D.
PA (CHIN-) CHINN J.
PA (DUFO-) DUFOUR G E.
PA (JACK-) JACKSON J L.
PA (YUUY-) YU J Y.
PA (TUAS-) TUASON O.
PA (YAP-) YAP P E.
PA (AMSH-) AMSHEY S R.
PA (DAMT-) DAM T C.
PA (LIUT-) LIU T F.
PA (GERS-) GERSTIN E H.
PA (PERA-) PERALTA C H.
PA (LEWI-) LEWIS S A.
PA (CHEN-) CHEN A J.
PA (MARW-) MARWAHA R.
PA (LANR-) LAN R Y.
PA (URAS-) URASHKA M E.
PA (KRIS-) KRISTNAM S R.
PA (KOLL-) KOLLURU V.
PA (PANE-) PANESAR I S.
Query Match 4.8%; Score 81.5; DB 7; Length 587;
Best Local Similarity 22.3%; Pred. No. 57;
RESULT 775
ID AAG30538 standard; protein; 725 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36527.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.8%; Score 81.5; DB 3; Length 725;
Best Local Similarity 20.6%; Pred. No. 77;
RESULT 776
ID AAG30537 standard; protein; 735 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36526.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.8%; Score 81.5; DB 3; Length 735;
Best Local Similarity 20.6%; Pred. No. 79;
RESULT 777
ID AAG30536 standard; protein; 778 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36525.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.8%; Score 81.5; DB 3; Length 778;
Best Local Similarity 20.6%; Pred. No. 86;
RESULT 778
ID ABU25347 standard; protein; 835 AA.
DE Protein encoded by Prokaryotic essential gene #10874.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 81.5; DB 6; Length 835;
Best Local Similarity 21.8%; Pred. No. 95;
RESULT 779
ID AAW22775 standard; protein; 1312 AA.
DE Human RAD50.
PN WO9727284-A2.
PD 31-JUL-1997.
PA (GENE-) GENELABS TECHNOLOGIES INC.
Query Match 4.8%; Score 81.5; DB 2; Length 1312;
Best Local Similarity 23.1%; Pred. No. 1.8e+02;
RESULT 780
ID ABG12816 standard; protein; 388 AA.
DE Novel human diagnostic protein #12807.
PN WO200175067-A2.

PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.8%; Score 81; DB 4; Length 388;
Best Local Similarity 23.0%; Pred. No. 35;
RESULT 781
ID AAR15507 standard; protein; 485 AA.
DE Tomato ACC synthase encoded by clone LE-ACC2.
PN USN7579896-N.
PD 12-NOV-1991.
PA (USDA) US SEC OF AGRIC.
Query Match 4.8%; Score 81; DB 2; Length 485;
Best Local Similarity 19.7%; Pred. No. 49;
RESULT 782
ID AAW47314 standard; protein; 485 AA.
DE Tomato ACC synthase LE-ACC2.
PN US5723766-A.
PD 03-MAR-1998.
PA (USDA) US SEC OF AGRIC.
Query Match 4.8%; Score 81; DB 2; Length 485;
Best Local Similarity 19.7%; Pred. No. 49;
RESULT 783
ID AAE00984 standard; protein; 485 AA.
DE Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2.
PN US6207881-B1.
PD 27-MAR-2001.
PA (USDA) US SEC OF AGRIC.
Query Match 4.8%; Score 81; DB 4; Length 485;
Best Local Similarity 19.7%; Pred. No. 49;
RESULT 784
ID AAB59720 standard; protein; 485 AA.
DE Protein encoded by tomato ACC synthase gene LE-ACC 2.
PN US6156956-A.
PD 05-DEC-2000.
PA (USDA) US DEPT OF AGRICULTURE.
Query Match 4.8%; Score 81; DB 4; Length 485;
Best Local Similarity 19.7%; Pred. No. 49;
RESULT 785
ID AAB59725 standard; protein; 485 AA.
DE Tomato ACC synthase gene LE-ACC2(b) clone.
PN US6156956-A.
PD 05-DEC-2000.
PA (USDA) US DEPT OF AGRICULTURE.
Query Match 4.8%; Score 81; DB 4; Length 485;
Best Local Similarity 19.7%; Pred. No. 49;
RESULT 786
ID ABU20678 standard; protein; 504 AA.
DE Protein encoded by Prokaryotic essential gene #6205.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.8%; Score 81; DB 6; Length 504;
Best Local Similarity 25.5%; Pred. No. 52;
RESULT 787
ID AAE01117 standard; protein; 552 AA.
DE Human gene 4 encoded secreted protein HSLH186, SEQ ID NO:31.
PN WO200134799-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 81; DB 4; Length 552;
Best Local Similarity 19.4%; Pred. No. 59;
RESULT 788
ID ABG64586 standard; protein; 552 AA.
DE Human albumin fusion protein #1261.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 81; DB 5; Length 552;
Best Local Similarity 19.4%; Pred. No. 59;
RESULT 789
ID ADL77853 standard; protein; 552 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1335.
PN US2004010134-A1.
PD 15-JAN-2004.

PA (ROSE/) ROSEN C A.
ID (HASE/) HASELTINE W A.
Query Match 4.8%; Score 81; DB 8; Length 552;
Best Local Similarity 19.4%; Pred. No. 59;
RESULT 790
ID AAB65970 standard; protein; 754 AA.
DE Human secreted protein BLAST search protein SEQ ID NO: 110.
PN WO200077023-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.8%; Score 81; DB 4; Length 754;
Best Local Similarity 20.0%; Pred. No. 92;
RESULT 791
ID ADS28536 standard; protein; 848 AA.
DE Bacterial polypeptide #17569.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.8%; Score 81; DB 8; Length 848;
Best Local Similarity 27.0%; Pred. No. 1.1e+02;
RESULT 792
ID ADR95699 standard; protein; 959 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4334.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 81; DB 8; Length 959;
Best Local Similarity 23.4%; Pred. No. 1.3e+02;
RESULT 793
ID ABU01981 standard; protein; 1032 AA.
DE S. pneumoniae type 4 strain protein from coding region #1558.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 4.8%; Score 81; DB 6; Length 1032;
Best Local Similarity 23.4%; Pred. No. 1.4e+02;
RESULT 794
ID ADK46851 standard; protein; 1032 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3366.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.8%; Score 81; DB 8; Length 1032;
Best Local Similarity 23.4%; Pred. No. 1.4e+02;
RESULT 795
ID AAW50898 standard; protein; 1609 AA.
DE Human laminin G1 chain.
PN WO9815179-A1.
PD 16-APR-1998.
PA (UNITW) UNIT WASHINGTON.
Query Match 4.8%; Score 81; DB 2; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.7e+02;
RESULT 796
ID ADL61261 standard; protein; 1609 AA.
DE Human protein tyrosine kinase biomarker laminin gamma 1 protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 4.8%; Score 81; DB 8; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.7e+02;
RESULT 797
ID ADR87632 standard; protein; 1609 AA.
DE Human laminin beta 2, SEQ ID 36.
PN WO2004075835-A2.
PD 10-SEP-2004.
PA (GETH) GEMENTECH INC.
Query Match 4.8%; Score 81; DB 8; Length 1609;
Best Local Similarity 22.1%; Pred. No. 2.7e+02;

RESULT 798
ID ADD55738 standard; protein; 661 AA.
DE Thalecress environmental stress-related protein #48.
PN US2003131386-A1.
PD 10-JUL-2003.
PA (SAMA/) SAMAHA R.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (KEDD/) KEDDIE J.
PA (RATC/) RATCLIFFE O.
PA (PIIG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (ZHAN/) ZHANG J.
Query Match 4.8%; Score 80.5; DB 7; Length 661;
Best Local Similarity 20.5%; Pred. No. 86;
RESULT 799
ID ADO01835 standard; protein; 661 AA.
DE Thalecress transcription factor protein #124.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PIIG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 4.8%; Score 80.5; DB 8; Length 661;
Best Local Similarity 20.5%; Pred. No. 86;
RESULT 800
ID ABB65439 standard; protein; 1377 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23109.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.8%; Score 80.5; DB 4; Length 1377;
Best Local Similarity 21.9%; Pred. No. 2.5e+02;
RESULT 801
ID ADC51662 standard; protein; 2273 AA.
DE Human MEGF8 protein #2.
PN JP2002360254-A.
PD 17-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 4.8%; Score 80.5; DB 7; Length 2273;
Best Local Similarity 34.2%; Pred. No. 5.1e+02;
RESULT 802
ID ADC51660 standard; protein; 2778 AA.
DE Human MEGF8 protein #1.
PN JP2002360254-A.
PD 17-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 4.8%; Score 80.5; DB 7; Length 2778;
Best Local Similarity 34.2%; Pred. No. 6.8e+02;
RESULT 803
ID ADG75733 standard; protein; 2789 AA.
DE Human protein modification and maintenance molecule polypeptide SeqID57.
PN WO2003083084-A2.

PD 09-OCT-2003.
PA (INCY-) INCYTE CORP.
Query Match 4.7%; Score 80.5; DB 7; Length 2789;
Best Local Similarity 34.2%; Pred. No. 6.8e+02;
RESULT 804
ID ABB82209 standard; protein; 213 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO83130, SEQ:5694.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.7%; Score 80; DB 8; Length 213;
Best Local Similarity 22.9%; Pred. No. 19;
RESULT 805
ID ADA35158 standard; protein; 305 AA.
DE Acinetobacter baumannii protein #2319.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 80; DB 6; Length 305;
Best Local Similarity 23.1%; Pred. No. 32;
RESULT 806
ID ABB63183 standard; protein; 575 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16341.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.7%; Score 80; DB 4; Length 575;
Best Local Similarity 25.9%; Pred. No. 79;
RESULT 807
ID ABG22494 standard; protein; 604 AA.
DE Novel human diagnostic protein #22485.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 80; DB 4; Length 604;
Best Local Similarity 20.4%; Pred. No. 85;
RESULT 808
ID AAR48627 standard; protein; 1122 AA.
DE Protein-tyrosine-kinase tek.
PN WO9404694-A1.
PD 03-MAR-1994.
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
Query Match 4.7%; Score 80; DB 2; Length 1122;
Best Local Similarity 20.3%; Pred. No. 2.1e+02;
RESULT 809
ID AAB19805 standard; protein; 1605 AA.
DE Mouse laminin 2 gamma-1 chain.
PN WO200066730-A2.
PD 09-NOV-2000.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 4.7%; Score 80; DB 3; Length 1605;
Best Local Similarity 22.5%; Pred. No. 3.5e+02;
RESULT 810
ID AAB48454 standard; protein; 1605 AA.
DE Mouse laminin 8 polypeptide, SEQ ID NO: 26.
PN WO200066732-A2.
PD 09-NOV-2000.
PA (BIOS-) BIOSTRATUM INC.
Query Match 4.7%; Score 80; DB 3; Length 1605;
Best Local Similarity 22.5%; Pred. No. 3.5e+02;
RESULT 811
ID ABB81596 standard; protein; 1605 AA.
DE Mouse laminin 10 third chain protein sequence SEQ ID NO:18.
PN WO200250111-A2.
PD 27-JUN-2002.
PA (BIOS-) BIOSTRATUM INC.
Query Match 4.7%; Score 80; DB 5; Length 1605;
Best Local Similarity 22.5%; Pred. No. 3.5e+02;
RESULT 812
ID ADT49890 standard; protein; 1605 AA.
DE Murine J02930 SEQ ID NO:97.
PN WO2004083241-A2.
PD 30-SEP-2004.

PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 4.7%; Score 80; DB 8; Length 1605;
Best Local Similarity 22.5%; Pred. No. 3.5e+02;
RESULT 813
ID ABU12113 standard; protein; 1887 AA.
DE Human protein modification and maintenance molecule (PMOD) #10.
PN WO200281636-A2.
PD 17-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 80; DB 6; Length 1887;
Best Local Similarity 26.3%; Pred. No. 4.4e+02;
RESULT 814
ID ABB80242 standard; protein; 1887 AA.
DE Human subtilase.
PN WO2003060109-A2.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 4.7%; Score 80; DB 7; Length 1887;
Best Local Similarity 26.3%; Pred. No. 4.4e+02;
RESULT 815
ID ADM29324 standard; protein; 1887 AA.
DE Human novel protein NOV10a.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 80; DB 7; Length 1887;
Best Local Similarity 26.3%; Pred. No. 4.4e+02;
RESULT 816
ID ADH48732 standard; protein; 2854 AA.
DE NOV7 protein sequence, SEQ ID 16.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.7%; Score 80; DB 5; Length 2854;
Best Local Similarity 31.7%; Pred. No. 8e+02;
RESULT 817
ID AAE38614 standard; protein; 395 AA.
DE Mouse thymidylate kinase protein.
PN WO2003064642-A1.
PD 07-AUG-2003.
PA (FARB) BAYER AG.
Query Match 4.7%; Score 79.5; DB 7; Length 395;
Best Local Similarity 21.3%; Pred. No. 52;
RESULT 818
ID ADJ76250 standard; protein; 395 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1502.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.7%; Score 79.5; DB 8; Length 395;
Best Local Similarity 21.3%; Pred. No. 52;
RESULT 819
ID ABU25076 standard; protein; 415 AA.
DE Protein encoded by Prokaryotic essential gene #10603.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.7%; Score 79.5; DB 6; Length 415;
Best Local Similarity 22.0%; Pred. No. 56;
RESULT 820
ID AAR15506 standard; protein; 485 AA.
DE Tomato ACC synthase encoded by clone ptACC1.
PN USN7579896-N.
PD 12-NOV-1991.
PA (USDA) US SEC OF AGRIC.
Query Match 4.7%; Score 79.5; DB 2; Length 485;
Best Local Similarity 22.6%; Pred. No. 70;
RESULT 821
ID AAW47313 standard; protein; 485 AA.
DE Tomato ACC synthase.
PN US5723766-A.
PD 03-MAR-1998.
PA (USDA) US SEC OF AGRIC.

Query Match 4.7%; Score 79.5; DB 2; Length 485;
Best Local Similarity 22.6%; Pred. No. 70;
RESULT 822
ID AAE00983 standard; protein; 485 AA.
DE Tomato-1-aminocyclopropane-1-carboxylic acid synthase (ACC).
PN US6207881-B1.
PD 27-MAR-2001.
PA (USDA) US SEC OF AGRIC.
Query Match 4.7%; Score 79.5; DB 4; Length 485;
Best Local Similarity 22.6%; Pred. No. 70;
RESULT 823
ID AAB59719 standard; protein; 485 AA.
DE Tomato ACC synthase.
PN US6156956-A.
PD 05-DEC-2000.
PA (USDA) US DEPT OF AGRICULTURE.
Query Match 4.7%; Score 79.5; DB 4; Length 485;
Best Local Similarity 22.6%; Pred. No. 70;
RESULT 824
ID ADR10465 standard; protein; 682 AA.
DE Human protein useful for treating neurological disease Seq 3971.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.7%; Score 79.5; DB 8; Length 682;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 825
ID AAG81808 standard; protein; 701 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:710.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match 4.7%; Score 79.5; DB 4; Length 701;
Best Local Similarity 21.9%; Pred. No. 1.2e+02;
RESULT 826
ID ABP38170 standard; protein; 703 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3015.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.7%; Score 79.5; DB 5; Length 703;
Best Local Similarity 21.9%; Pred. No. 1.2e+02;
RESULT 827
ID ADS04687 standard; protein; 703 AA.
DE Staphylococcus epidermis polypeptide seqid 3982.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 4.7%; Score 79.5; DB 8; Length 703;
Best Local Similarity 21.9%; Pred. No. 1.2e+02;
RESULT 828
ID AAO16642 standard; protein; 919 AA.
DE Human extracellular messenger protein #2.
PN WO2003002610-A1.
PD 09-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.7%; Score 79.5; DB 6; Length 919;
Best Local Similarity 24.3%; Pred. No. 1.8e+02;
RESULT 829
ID ADI27626 standard; protein; 919 AA.
DE Human SCUBE2 protein.
PN US2003219813-A1.
PD 27-NOV-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.7%; Score 79.5; DB 8; Length 919;
Best Local Similarity 24.3%; Pred. No. 1.8e+02;
RESULT 830
ID ADQ66056 standard; protein; 971 AA.
DE Novel human protein sequence #1029.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Query Match 4.7%; Score 79.5; DB 8; Length 971;
Best Local Similarity 24.3%; Pred. No. 1.9e+02;
RESULT 831
ID ABP69329 standard; protein; 999 AA.
DE Human polypeptide SEQ ID NO 1376.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.7%; Score 79.5; DB 5; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 832
ID ABG61893 standard; protein; 999 AA.
DE Prostate cancer-associated protein #94.
PN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 5; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 833
ID ABB80926 standard; protein; 999 AA.
DE Human breast cancer modulating protein BCO2.
PN WO200255988-A2.
PD 18-JUL-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 5; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 834
ID ABJ05567 standard; protein; 999 AA.
DE Breast cancer-associated protein 32.
PN WO200259377-A2.
PD 01-AUG-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 5; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 835
ID ABJ19815 standard; protein; 999 AA.
DE Androgen-independent prostate cancer-related protein - SEQ ID NO 42.
PN WO200298358-A2.
PD 12-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 6; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 836
ID ABR47407 standard; protein; 999 AA.
DE Breast cancer associated protein sequence SEQ ID NO:45.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.7%; Score 79.5; DB 6; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 837
ID ADN39416 standard; protein; 999 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A16.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 7; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 838
ID ADN38734 standard; protein; 999 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:52.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 7; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 839
ID ADN39569 standard; protein; 999 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:A169.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.7%; Score 79.5; DB 7; Length 999;

Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 840
ID ADI27636 standard; protein; 999 AA.
DE SCUBE2 homologous protein.
PN US2003219813-A1.
PD 27-NOV-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.7%; Score 79.5; DB 8; Length 999;
Best Local Similarity 24.3%; Pred. No. 2e+02;
RESULT 841
ID AAR53146 standard; protein; 1117 AA.
DE Mouse tyrosine kinase ("tek") expressed during cardiogenesis.
PN CA2085291-A.
PD 31-JAN-1994.
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
Query Match 4.7%; Score 79.5; DB 2; Length 1117;
Best Local Similarity 20.0%; Pred. No. 2.3e+02;
RESULT 842
ID ADP47905 standard; protein; 1866 AA.
DE Human inflammation/cancer-related CATERPILLER NOD27 protein.
PN WO2004034093-A2.
PD 22-APR-2004.
PA (UYNC-) UNIV NORTH CAROLINA.
Query Match 4.7%; Score 79.5; DB 8; Length 1866;
Best Local Similarity 23.0%; Pred. No. 4.9e+02;
RESULT 843
ID ADP12959 standard; protein; 1866 AA.
DE Protein encoding reference mRNA sequence #44.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 4.7%; Score 79.5; DB 8; Length 1866;
Best Local Similarity 23.0%; Pred. No. 4.9e+02;
RESULT 844
ID AAB38635 standard; protein; 251 AA.
DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:172.
PN WO200056882-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 79; DB 3; Length 251;
Best Local Similarity 21.0%; Pred. No. 31;
RESULT 845
ID AAB38633 standard; protein; 259 AA.
DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:170.
PN WO200056882-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 79; DB 3; Length 259;
Best Local Similarity 21.0%; Pred. No. 32;
RESULT 846
ID AAB38631 standard; protein; 259 AA.
DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:168.
PN WO200056882-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 79; DB 3; Length 259;
Best Local Similarity 21.0%; Pred. No. 32;
RESULT 847
ID AAB38629 standard; protein; 259 AA.
DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:166.
PN WO200056882-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 79; DB 3; Length 259;
Best Local Similarity 21.0%; Pred. No. 32;
RESULT 848
ID ADR41503 standard; protein; 565 AA.
DE Human CD-1like molecule HFKFH60, SEQ ID NO:302.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.7%; Score 79; DB 5; Length 565;
Best Local Similarity 21.0%; Pred. No. 98;

RESULT 849
ID ABM83037 standard; protein; 889 AA.
DE Human diagnostic and therapeutic protein SEQ ID NO:3286.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.7%; Score 79; DB 8; Length 889;
Best Local Similarity 24.5%; Pred. No. 1.9e+02;
RESULT 850
ID AAY59046 standard; protein; 1118 AA.
DE Mouse receptor tyrosine kinase protein.
PN US5998187-A.
PD 07-DEC-1999.
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
Query Match 4.7%; Score 79; DB 3; Length 1118;
Best Local Similarity 20.3%; Pred. No. 2.6e+02;
RESULT 851
ID AAY59048 standard; protein; 1122 AA.
DE Mouse tek receptor tyrosine kinase protein.
PN US5998187-A.
PD 07-DEC-1999.
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
Query Match 4.7%; Score 79; DB 3; Length 1122;
Best Local Similarity 20.3%; Pred. No. 2.6e+02;
RESULT 852
ID AAR73951 standard; protein; 1123 AA.
DE Mouse tie-2 receptor tyrosine kinase protein.
PN WO9513387-A1.
PD 18-MAY-1995.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 4.7%; Score 79; DB 2; Length 1123;
Best Local Similarity 20.3%; Pred. No. 2.6e+02;
RESULT 853
ID AAR67391 standard; protein; 1123 AA.
DE Murine tyrosine kinase receptor tie-2.
PN JP06315382-A.
PD 15-NOV-1994.
PA (SUDA/) SUDA T.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
Query Match 4.7%; Score 79; DB 2; Length 1123;
Best Local Similarity 20.3%; Pred. No. 2.6e+02;
RESULT 854
ID ABU07840 standard; protein; 1125 AA.
DE Murine Tie receptor tyrosine kinase 2 (Tie 2).
PN WO2003004529-A2.
PD 16-JAN-2003.
PA (LICN) LICENTIA LTD.
Query Match 4.7%; Score 79; DB 6; Length 1125;
Best Local Similarity 20.3%; Pred. No. 2.6e+02;
RESULT 855
ID AAY14208 standard; peptide; 229 AA.
DE HIV-1 gp120 peptide.
PN WO9924065-A1.
PD 20-MAY-1999.
PA (UYCO) UNIV COLUMBIA NEW YORK.
PA (DAND) DANA FARBER CANCER INST INC.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 4.6%; Score 78.5; DB 2; Length 229;
Best Local Similarity 25.7%; Pred. No. 30;
RESULT 856
ID AAY14212 standard; peptide; 229 AA.
DE HIV gp120 protein fragment.
PN WO9924553-A2.
PD 20-MAY-1999.
PA (UYCO) UNIV COLUMBIA NEW YORK.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 4.6%; Score 78.5; DB 2; Length 229;
Best Local Similarity 25.7%; Pred. No. 30;
RESULT 857
ID ABG22503 standard; protein; 410 AA.
DE Novel human diagnostic protein #22494.
PN WO200175067-A2.
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 78.5; DB 4; Length 410;
Best Local Similarity 20.5%; Pred. No. 70;
RESULT 858
ID AAB07666 standard; protein; 785 AA.
DE Amino acid sequence of TARI, a surface layer protein.
PN EPI026248-A2.
PD 09-AUG-2000.
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
Query Match 4.6%; Score 78.5; DB 3; Length 785;
Best Local Similarity 21.8%; Pred. No. 1.8e+02;
RESULT 859
ID ABB65359 standard; protein; 1087 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22869.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 78.5; DB 4; Length 1087;
Best Local Similarity 22.3%; Pred. No. 2.8e+02;
RESULT 860
ID ABB65358 standard; protein; 1087 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22866.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 78.5; DB 4; Length 1087;
Best Local Similarity 22.3%; Pred. No. 2.8e+02;
RESULT 861
ID AAW71295 standard; protein; 1312 AA.
DE Human homologue of yeast RAD50.
PN WO9838306-A1.
PD 03-SEP-1998.
PA (GENE-) GENELABS TECHNOLOGIES INC.
Query Match 4.6%; Score 78.5; DB 2; Length 1312;
Best Local Similarity 22.5%; Pred. No. 3.7e+02;
RESULT 862
ID ABG30373 standard; protein; 356 AA.
DE Novel human diagnostic protein #30364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 78; DB 4; Length 356;
Best Local Similarity 20.0%; Pred. No. 64;
RESULT 863
ID ADM99266 standard; protein; 408 AA.
DE Cochliobolus heterostrophus strain C4 protease protein SeqID 149.
PN WO2004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 4.6%; Score 78; DB 8; Length 408;
Best Local Similarity 22.0%; Pred. No. 78;
RESULT 864
ID ADM99268 standard; protein; 408 AA.
DE Cochliobolus heterostrophus strain C4 protease protein SeqID 151.
PN WO2004033668-A2.
PD 22-APR-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 4.6%; Score 78; DB 8; Length 408;
Best Local Similarity 22.0%; Pred. No. 78;
RESULT 865
ID AAB13632 standard; protein; 880 AA.
DE C. trachomatis pmp1 gene protein.
PN WO200034483-A2.
PD 15-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match 4.6%; Score 78; DB 3; Length 880;
Best Local Similarity 23.5%; Pred. No. 2.4e+02;
RESULT 866
ID AAG83200 standard; protein; 880 AA.
DE Protein encoded by Chlamydia trachomatis pmp1 gene.
PN WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.

Query Match 4.6%; Score 78; DB 4; Length 880;
Best Local Similarity 23.5%; Pred. No. 2.4e+02;
RESULT 867
ID ABB94171 standard; protein; 880 AA.
DE Chlamydia protein sequence SEQ ID NO:175.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.6%; Score 78; DB 5; Length 880;
Best Local Similarity 23.5%; Pred. No. 2.4e+02;
RESULT 868
ID ADI62841 standard; protein; 324 AA.
DE Rat Protein P97578, SEQ ID NO 8775.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.6%; Score 77.5; DB 7; Length 324;
Best Local Similarity 20.8%; Pred. No. 63;
RESULT 869
ID ABG61528 standard; protein; 363 AA.
DE Iron uptake ABC transporter polypeptide #35.
PN WO200234773-A2.
PD 02-MAY-2002.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match 4.6%; Score 77.5; DB 5; Length 363;
Best Local Similarity 19.9%; Pred. No. 74;
RESULT 870
ID ADN27279 standard; protein; 394 AA.
DE Bacterial polypeptide #9932.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.6%; Score 77.5; DB 8; Length 394;
Best Local Similarity 27.3%; Pred. No. 84;
RESULT 871
ID ADA84087 standard; protein; 414 AA.
DE Human HHLA2 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 4.6%; Score 77.5; DB 6; Length 414;
Best Local Similarity 16.7%; Pred. No. 90;
RESULT 872
ID ADQ80374 standard; protein; 414 AA.
DE HERV-H LTR-associating 2 protein.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 4.6%; Score 77.5; DB 8; Length 414;
Best Local Similarity 16.7%; Pred. No. 90;
RESULT 873
ID AAU79177 standard; protein; 425 AA.
DE Mouse tandem PH-domain-containing protein-2 (TAPP2) protein.
PN WO200212276-A2.
PD 14-FEB-2002.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 4.6%; Score 77.5; DB 5; Length 425;
Best Local Similarity 21.8%; Pred. No. 93;
RESULT 874
ID ABR40241 standard; protein; 425 AA.
DE Murine TAPP2.
PN WO2003011901-A1.
PD 13-FEB-2003.
PA (UYDU-) UNIV DUNDEE.
Query Match 4.6%; Score 77.5; DB 6; Length 425;
Best Local Similarity 21.8%; Pred. No. 93;
RESULT 875
ID ADJ95156 standard; protein; 451 AA.

DE Novel NOVX protein sequence #192.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.6%; Score 77.5; DB 7; length 451;
Best Local Similarity 26.0%; Pred. No. 1e+02;
RESULT 876
ID AAR31186 standard; protein; 462 AA.
DE GABA-A receptor alpha-5 subunit.
PN WO9222652-A1.
PD 23-DEC-1992.
PA (MERI) MERCK SHARP & DOHME LTD.
Query Match 4.6%; Score 77.5; DB 2; length 462;
Best Local Similarity 26.0%; Pred. No. 1.1e+02;
RESULT 877
ID AAR59864 standard; protein; 462 AA.
DE Human GABA receptor alphas subunit.
PN WO9413799-A1.
PD 23-JUN-1994.
PA (MERI) MERCK SHARP & DOHME LTD.
Query Match 4.6%; Score 77.5; DB 2; length 462;
Best Local Similarity 26.0%; Pred. No. 1.1e+02;
RESULT 878
ID ADB78624 standard; protein; 462 AA.
DE Human GABA receptor subunit mutant SEQ ID NO:168.
PN WO2003008574-A1.
PD 30-JAN-2003.
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
Query Match 4.6%; Score 77.5; DB 7; length 462;
Best Local Similarity 26.0%; Pred. No. 1.1e+02;
RESULT 879
ID AAW26428 standard; protein; 530 AA.
DE Swinepox virus HindIII C encoded protein C18L.
PN US5651972-A.
PD 29-JUL-1997.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 4.6%; Score 77.5; DB 2; length 530;
Best Local Similarity 24.3%; Pred. No. 1.3e+02;
RESULT 880
ID AAB68249 standard; protein; 530 AA.
DE Protein encoded by reverse complement of HindIII C fragment of SPV.
PN US6217882-B1.
PD 17-APR-2001.
PA (UYFL) UNIV FLORIDA RES FOUND INC.
Query Match 4.6%; Score 77.5; DB 4; length 530;
Best Local Similarity 24.3%; Pred. No. 1.3e+02;
RESULT 881
ID AAG92916 standard; protein; 657 AA.
DE C glucumicum protein fragment SEQ ID NO: 6670.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 4.6%; Score 77.5; DB 4; length 657;
Best Local Similarity 20.4%; Pred. No. 1.7e+02;
RESULT 882
ID ABB93142 standard; protein; 669 AA.
DE Herbicidially active polypeptide SEQ ID NO 2353.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.6%; Score 77.5; DB 5; length 669;
Best Local Similarity 23.3%; Pred. No. 1.8e+02;
RESULT 883
ID ADJ76177 standard; protein; 761 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1429.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.6%; Score 77.5; DB 8; length 761;
Best Local Similarity 21.8%; Pred. No. 2.2e+02;
RESULT 884
ID AAU79822 standard; protein; 838 AA.

DE OSF-2 protein associated protein #1.
PN WO200220055-A1.
PD 14-MAR-2002.
PA (SUNR) SUNTORY LTD.
PA (SUNR) SUNTORY BIOMEDICAL RES LTD.
Query Match 4.6%; Score 77.5; DB 5; length 838;
Best Local Similarity 19.8%; Pred. No. 2.5e+02;
RESULT 885
ID ABU48219 standard; protein; 890 AA.
DE Protein encoded by Prokaryotic essential gene #33746.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.6%; Score 77.5; DB 6; length 890;
Best Local Similarity 22.4%; Pred. No. 2.7e+02;
RESULT 886
ID ABG22502 standard; protein; 1016 AA.
DE Novel human diagnostic protein #22493.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.6%; Score 77.5; DB 4; length 1016;
Best Local Similarity 22.1%; Pred. No. 3.3e+02;
RESULT 887
ID ABB61252 standard; protein; 1078 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 10548.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.6%; Score 77.5; DB 4; length 1078;
Best Local Similarity 20.0%; Pred. No. 3.6e+02;
RESULT 888
ID AAY41654 standard; protein; 210 AA.
DE Zea mays XIAP associated factor 1 protein.
PN WO9947688-A1.
PD 23-SEP-1999.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 4.5%; Score 77; DB 2; length 210;
Best Local Similarity 26.0%; Pred. No. 38;
RESULT 889
ID ABU49577 standard; protein; 330 AA.
DE Protein encoded by Prokaryotic essential gene #35104.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.5%; Score 77; DB 6; length 330;
Best Local Similarity 20.9%; Pred. No. 73;
RESULT 890
ID AAR83406 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant N89Q + N247Q.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.5%; Score 77; DB 2; length 402;
Best Local Similarity 18.2%; Pred. No. 97;
RESULT 891
ID ADH87596 standard; protein; 489 AA.
DE Enterococcus faecalis polypeptide #2076.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 4.5%; Score 77; DB 7; length 489;
Best Local Similarity 20.4%; Pred. No. 1.3e+02;
RESULT 892
ID ABM68570 standard; protein; 600 AA.
DE Photorhabdus luminescens protein sequence #1667.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.5%; Score 77; DB 6; length 600;
Best Local Similarity 24.8%; Pred. No. 1.7e+02;

RESULT 893
ID ADH09924 standard; protein; 620 AA.
DE Human host factor protein, SEQ ID No 452.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 620;
Pred. No. 1.8e+02;
RESULT 894
ID ADN19438 standard; protein; 789 AA.
DE Bacterial polypeptide #2091.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 789;
Pred. No. 2.6e+02;
RESULT 895
ID AAB58428 standard; protein; 848 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 766.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match
Best Local Similarity 4.5%; Score 77; DB 3; Length 848;
Pred. No. 2.8e+02;
RESULT 896
ID ABR64269 standard; protein; 858 AA.
DE Angiogenesis protein BNO367.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match
Best Local Similarity 4.5%; Score 77; DB 6; Length 858;
Pred. No. 2.9e+02;
RESULT 897
ID ADE54205 standard; protein; 858 AA.
DE Human Protein Q92598, SEQ ID NO 8.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 858;
Pred. No. 2.9e+02;
RESULT 898
ID ADE54209 standard; protein; 858 AA.
DE Human Protein Q92598, SEQ ID NO 12.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 858;
Pred. No. 2.9e+02;
RESULT 899
ID ADH09935 standard; protein; 858 AA.
DE Human host factor protein, SEQ ID No 463.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 858;
Pred. No. 2.9e+02;
RESULT 900
ID ADH09936 standard; protein; 858 AA.
DE Human host factor protein, SEQ ID No 464.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 858;
Pred. No. 2.9e+02;
RESULT 901
ID ADH09925 standard; protein; 858 AA.

DE Human host factor protein, SEQ ID No 453.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 858;
Pred. No. 2.9e+02;
RESULT 902
ID ADL22530 standard; protein; 858 AA.
DE Human cancer antigen-related hsp105 protein.
PN WO2004020624-A1.
PD 11-MAR-2004.
PA (KUMA-) KUMAMOTO TECHNOLOGY & IND FOUND.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 858;
Pred. No. 2.9e+02;
RESULT 903
ID AAY07110 standard; protein; 872 AA.
DE Colon cancer associated antigen precursor sequence.
PN WO9904265-A2.
PD 28-JAN-1999.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 4.5%; Score 77; DB 2; Length 872;
Pred. No. 3e+02;
RESULT 904
ID ADH09926 standard; protein; 872 AA.
DE Human host factor protein, SEQ ID No 454.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 872;
Pred. No. 3e+02;
RESULT 905
ID ABG91020 standard; protein; 878 AA.
DE Chlamydia trachomatis outer membrane protein I protein.
PN WO200262380-A2.
PD 15-AUG-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 4.5%; Score 77; DB 5; Length 878;
Pred. No. 3e+02;
RESULT 906
ID AAE23454 standard; protein; 878 AA.
DE Chlamydia trachomatis l2 PMPI protein.
PN WO200228998-A2.
PD 11-APR-2002.
PA (ANTE-) ANTEX BIOLOGICS INC.
Query Match
Best Local Similarity 4.5%; Score 77; DB 5; Length 878;
Pred. No. 3e+02;
RESULT 907
ID ADD43790 standard; protein; 878 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 85.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 878;
Pred. No. 3e+02;
RESULT 908
ID ADD43792 standard; protein; 878 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 87.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 878;
Pred. No. 3e+02;
RESULT 909
ID ADP43728 standard; protein; 878 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 23.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 878;
Pred. No. 3e+02;
RESULT 910
ID ADP43712 standard; protein; 878 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 7.

PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 878;
Pred. No. 3e+02;
RESULT 911
ID ABE19855 standard; protein; 1018 AA.
DE Novel human diagnostic protein #19846.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.5%; Score 77; DB 4; Length 1018;
Pred. No. 3.7e+02;
RESULT 912
ID ADE62754 standard; protein; 1085 AA.
DE Human Protein NP_005063, SEQ ID NO 8687.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 1085;
Pred. No. 4.1e+02;
RESULT 913
ID ADE62758 standard; protein; 1085 AA.
DE Human Protein NP_005063, SEQ ID NO 8691.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 1085;
Pred. No. 4.1e+02;
RESULT 914
ID ADE62762 standard; protein; 1085 AA.
DE Human Protein NP_005063, SEQ ID NO 8695.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.5%; Score 77; DB 7; Length 1085;
Pred. No. 4.1e+02;
RESULT 915
ID ABE81779 standard; protein; 1085 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO4814, SEQ.4582.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 4.5%; Score 77; DB 8; Length 1085;
Pred. No. 4.1e+02;
RESULT 916
ID AAM83160 standard; protein; 1101 AA.
DE Rat orphan tyrosine kinase receptor protein Rck-7 (Tie-2).
PN US5843749-A.
PD 01-DEC-1998.
PA (REGF-) REGENERON PHARM INC.
Query Match
Best Local Similarity 4.5%; Score 77; DB 2; Length 1101;
Pred. No. 4.1e+02;
RESULT 917
ID AAG45613 standard; protein; 1293 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57287.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.5%; Score 77; DB 3; Length 1293;
Pred. No. 5.2e+02;
RESULT 918
ID AAG45612 standard; protein; 1304 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57286.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.5%; Score 77; DB 3; Length 1304;
Pred. No. 5.3e+02;
RESULT 919
ID AAG45611 standard; protein; 1324 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 57285.

PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.5%; Score 77; DB 3; Length 1324;
Pred. No. 5.4e+02;
RESULT 920
ID AAM19784 standard; protein; 1726 AA.
DE Human multiple regulatory protein SPT6.
PN WO9703087-A1.
PD 30-JAN-1997.
PA (UNMI-) UNIV MICHIGAN.
Query Match
Best Local Similarity 4.5%; Score 77; DB 2; Length 1726;
Pred. No. 7.9e+02;
RESULT 921
ID AAU17511 standard; protein; 131 AA.
DE Novel signal transduction pathway protein, Seq ID 1076.
PN WO200154733-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.5%; Score 76.5; DB 4; Length 131;
Pred. No. 22;
RESULT 922
ID ABO27216 standard; protein; 131 AA.
DE Human signal transduction pathway component HMCFB47.
PN US2003036505-A1.
PD 20-FEB-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.5%; Score 76.5; DB 6; Length 131;
Pred. No. 22;
RESULT 923
ID ADB94219 standard; protein; 131 AA.
DE Human novel protein #453.
PN US2002168711-A1.
PD 14-NOV-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 4.5%; Score 76.5; DB 7; Length 131;
Pred. No. 22;
RESULT 924
ID AAG38906 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48065.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.5%; Score 76.5; DB 3; Length 287;
Pred. No. 67;
RESULT 925
ID AAG38905 standard; protein; 305 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48064.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.5%; Score 76.5; DB 3; Length 305;
Pred. No. 74;
RESULT 926
ID AAG38904 standard; protein; 312 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48063.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.5%; Score 76.5; DB 3; Length 312;
Pred. No. 76;
RESULT 927
ID AAG05059 standard; protein; 383 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1320.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.5%; Score 76.5; DB 3; Length 383;
Pred. No. 1e+02;
RESULT 928
ID ABO63725 standard; protein; 396 AA.
DE Klebsiella pneumoniae polypeptide seqid 10242.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 4.5%; Score 76.5; DB 7; Length 396;

Best Local Similarity 25.0%; Pred. No. 1.1e+02;
RESULT 929
ID AAB80371 standard; protein; 414 AA.
DE Secreted protein encoded by gene #1.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.5%; Score 76.5; DB 4; Length 414;
Best Local Similarity 16.7%; Pred. No. 1.1e+02;
RESULT 930
ID ABG65290 standard; protein; 414 AA.
DE Human albumin fusion protein #1965.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.5%; Score 76.5; DB 5; Length 414;
Best Local Similarity 16.7%; Pred. No. 1.1e+02;
RESULT 931
ID ADL78557 standard; protein; 414 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 2039.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 4.5%; Score 76.5; DB 8; Length 414;
Best Local Similarity 16.7%; Pred. No. 1.1e+02;
RESULT 932
ID AAG05058 standard; protein; 449 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1319.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.5%; Score 76.5; DB 3; Length 449;
Best Local Similarity 21.3%; Pred. No. 1.3e+02;
RESULT 933
ID AAG05057 standard; protein; 462 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1318.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.5%; Score 76.5; DB 3; Length 462;
Best Local Similarity 21.3%; Pred. No. 1.3e+02;
RESULT 934
ID AAB38626 standard; protein; 471 AA.
DE Gene 38 human secreted protein homologous amino acid sequence #163.
PN WO200056882-A1.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.5%; Score 76.5; DB 3; Length 471;
Best Local Similarity 19.3%; Pred. No. 1.4e+02;
RESULT 935
ID ADA55549 standard; protein; 570 AA.
DE Human protein, SEQ ID 3117.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.5%; Score 76.5; DB 6; Length 570;
Best Local Similarity 20.5%; Pred. No. 1.8e+02;
RESULT 936
ID ADJ70708 standard; protein; 570 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID2514.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.5%; Score 76.5; DB 7; Length 570;
Best Local Similarity 20.5%; Pred. No. 1.8e+02;
RESULT 937
ID AAR32657 standard; protein; 657 AA.
DE PSI protein from C.melasscola ATCC 17965.
PN WO9303158-A1.
PD 18-FEB-1993.
PA (ORSA-) ORSAN.
Query Match 4.5%; Score 76.5; DB 2; Length 657;

Best Local Similarity 20.4%; Pred. No. 2.2e+02;
RESULT 938
ID ADM29350 standard; protein; 753 AA.
DE Human novel protein NOV19a.
PN WO2003064628-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.5%; Score 76.5; DB 7; Length 753;
Best Local Similarity 21.7%; Pred. No. 2.7e+02;
RESULT 939
ID ADQ59433 standard; protein; 967 AA.
DE Human cancer-associated (CA) protein sequence SEQ ID NO:69.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 4.5%; Score 76.5; DB 8; Length 967;
Best Local Similarity 19.3%; Pred. No. 3.9e+02;
RESULT 940
ID ADN19491 standard; protein; 1000 AA.
DE Bacterial polypeptide #2144.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.5%; Score 76.5; DB 8; Length 1000;
Best Local Similarity 26.4%; Pred. No. 4.1e+02;
RESULT 941
ID ABB61540 standard; protein; 1191 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11412.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.5%; Score 76.5; DB 4; Length 1191;
Best Local Similarity 19.8%; Pred. No. 5.2e+02;
RESULT 942
ID ADH48824 standard; protein; 1356 AA.
DE NOV45B protein sequence, SEQ ID 108.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.5%; Score 76.5; DB 5; Length 1356;
Best Local Similarity 21.3%; Pred. No. 6.3e+02;
RESULT 943
ID ABB64069 standard; protein; 2009 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18999.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.5%; Score 76.5; DB 4; Length 2009;
Best Local Similarity 21.0%; Pred. No. 1.1e+03;
RESULT 944
ID ADJ11680 standard; protein; 265 AA.
DE Rice protein modulated by post-transcriptional gene silencing SegID 316.
PN US2003135888-A1.
PD 17-JUL-2003.
PA (ZHU/) ZHU T.
PA (WANG/) WANG X.
PA (CHAN/) CHANG H.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICHKE D.
Query Match 4.5%; Score 76; DB 7; Length 265;
Best Local Similarity 19.1%; Pred. No. 68;

ID ABU15068 standard; protein; 277 AA.
DE Protein encoded by Prokaryotic essential gene #595.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.5%; Score 76; DB 6; Length 277;
Best Local Similarity 23.6%; Pred. No. 72;
RESULT 946
ID ABG30302 standard; protein; 315 AA.
DE Novel human diagnostic protein #30293.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.5%; Score 76; DB 4; Length 315;
Best Local Similarity 22.3%; Pred. No. 87;
RESULT 947
ID ABU10305 standard; protein; 357 AA.
DE Chicken bves (cbves) carboxyl domain.
PN US6503540-B1.
PD 07-JAN-2003.
PA (REES/) REESE D E.
PA (BADE/) BADER D M.
Query Match 4.5%; Score 76; DB 7; Length 357;
Best Local Similarity 23.2%; Pred. No. 1e+02;
RESULT 948
ID ABB49335 standard; protein; 375 AA.
DE Listeria monocytogenes protein #2039.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 4.5%; Score 76; DB 5; Length 375;
Best Local Similarity 22.2%; Pred. No. 1.1e+02;
RESULT 949
ID ABG10732 standard; protein; 380 AA.
DE Novel human diagnostic protein #10723.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.5%; Score 76; DB 4; Length 380;
Best Local Similarity 19.8%; Pred. No. 1.1e+02;
RESULT 950
ID AAR83416 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant I310D.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.5%; Score 76; DB 2; Length 402;
Best Local Similarity 18.5%; Pred. No. 1.2e+02;
RESULT 951
ID ABB61459 standard; protein; 450 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11169.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.5%; Score 76; DB 4; Length 450;
Best Local Similarity 19.7%; Pred. No. 1.5e+02;
RESULT 952
ID ABP39455 standard; protein; 462 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4300.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.5%; Score 76; DB 5; Length 462;
Best Local Similarity 23.5%; Pred. No. 1.5e+02;
RESULT 953
ID ADS05296 standard; protein; 462 AA.
DE Staphylococcus epidermis polypeptide seqid 4591.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 4.5%; Score 76; DB 8; Length 462;
Best Local Similarity 23.5%; Pred. No. 1.5e+02;
RESULT 954
ID ABU10301 standard; protein; 487 AA.
DE Fragment of chicken bves (cbves).
PN US6503540-B1.
PD 07-JAN-2003.
PA (REES/) REESE D E.
PA (BADE/) BADER D M.
Query Match 4.5%; Score 76; DB 7; Length 487;
Best Local Similarity 23.2%; Pred. No. 1.6e+02;
RESULT 955
ID AAB00158 standard; protein; 507 AA.
DE BCD4-SCFv(17b) HIV single chain antibody fusion protein.
PN WO200055207-A1.
PD 21-SEP-2000.
PA (USSH) US NAT INST OF HEALTH.
Query Match 4.5%; Score 76; DB 3; Length 507;
Best Local Similarity 27.8%; Pred. No. 1.7e+02;
RESULT 956
ID AAY37049 standard; protein; 518 AA.
DE Protein involved in intermediate metabolism of sugars and/or cofactors.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 4.5%; Score 76; DB 2; Length 518;
Best Local Similarity 20.8%; Pred. No. 1.8e+02;
RESULT 957
ID ABB61505 standard; protein; 608 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11307.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.5%; Score 76; DB 4; Length 608;
Best Local Similarity 18.8%; Pred. No. 2.2e+02;
RESULT 958
ID ADR05763 standard; protein; 770 AA.
DE Mouse Notch2-like protein.
PN US2004152120-A1.
PD 05-AUG-2004.
PA (APPL-) APPLERA CORP.
Query Match 4.5%; Score 76; DB 8; Length 770;
Best Local Similarity 20.2%; Pred. No. 3.1e+02;
RESULT 959
ID ADN26806 standard; protein; 783 AA.
DE Bacterial polypeptide #9459.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.5%; Score 76; DB 2; Length 783;
Best Local Similarity 27.1%; Pred. No. 3.2e+02;
RESULT 960
ID AAR41867 standard; protein; 811 AA.
DE Mouse OSF-2.
PN EP562508-A2.
PD 29-SEP-1993.
PA (FARH) HOECHST JAPAN LTD.
Query Match 4.5%; Score 76; DB 5; Length 811;
Best Local Similarity 20.5%; Pred. No. 3.4e+02;
RESULT 961
ID AAU79824 standard; protein; 811 AA.
DE OSF-2 protein associated protein #2.
PN WO200220055-A1.
PD 14-MAR-2002.
PA (SUNR) SUNTORY BIOMEDICAL RES LTD.
PA (SUNR) SUNTORY BIOMEDICAL RES LTD.
Query Match 4.5%; Score 76; DB 5; Length 811;
Best Local Similarity 20.5%; Pred. No. 3.4e+02;
RESULT 962
ID ADJ76125 standard; protein; 811 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1377.

PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.5%; Score 76; DB 8; Length 811;
Best Local Similarity 20.5%; Pred. No. 3.4e+02;
RESULT 963
ID ADN19903 standard; protein; 1474 AA.
DE Bacterial polypeptide #2556.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.5%; Score 76; DB 8; Length 1474;
Best Local Similarity 21.4%; Pred. No. 8e+02;
RESULT 964
ID ABR47539 standard; protein; 1855 AA.
DE Breast cancer associated protein sequence SEQ ID NO:315.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.5%; Score 76; DB 6; Length 1855;
Best Local Similarity 22.8%; Pred. No. 1.1e+03;
RESULT 965
ID ADN04056 standard; protein; 1855 AA.
DE Antipsoriatic protein sequence #223.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 76; DB 8; Length 1855;
Best Local Similarity 22.8%; Pred. No. 1.1e+03;
RESULT 966
ID AAU04090 standard; protein; 2008 AA.
DE Human cadherin-like asymmetry protein, CLASP-4.
PN WO200142294-A2.
PD 14-JUN-2001.
PA (ARBO-) ARBOR VITA CORP.
Query Match 4.5%; Score 76; DB 4; Length 2008;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 967
ID ABG61703 standard; protein; 2008 AA.
DE Human cadherin-like asymmetry protein-4 (CLASP-4).
PN WO200231117-A2.
PD 18-APR-2002.
PA (ARBO-) ARBOR VITA CORP.
PA (GARM/) GARMAN J D.
PA (CAND/) CANDIA A F.
Query Match 4.5%; Score 76; DB 5; Length 2008;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 968
ID ABR43636 standard; protein; 2008 AA.
DE Human CLASP-4 protein SEQ ID NO:29.
PN WO2003025120-A2.
PD 27-MAR-2003.
PA (ARBO-) ARBOR VITA CORP.
Query Match 4.5%; Score 76; DB 6; Length 2008;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 969
ID ADC79417 standard; protein; 2008 AA.
DE Human CLASP-4 full-length protein.
PN US2002068302-A1.
PD 06-JUN-2002.
PA (LUPS/) LU P S.
PA (GARM/) GARMAN J D.
PA (CAND/) CANDIA A F.
Query Match 4.5%; Score 76; DB 7; Length 2008;
Best Local Similarity 17.2%; Pred. No. 1.2e+03;
RESULT 970
ID ABB59371 standard; protein; 4601 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 4905.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.5%; Score 76; DB 4; Length 4601;
Best Local Similarity 26.1%; Pred. No. 4.1e+03;
RESULT 971
ID ABB44610 standard; protein; 137 AA.
DE Human wound healing related polypeptide SEQ ID NO 93.
PN CA2325226-A1.
PD 17-MAY-2001.
PA (SWIT-) SWITCH BIOTECH AG.
Query Match 4.5%; Score 75.5; DB 4; Length 137;
Best Local Similarity 29.5%; Pred. No. 30;
RESULT 972
ID ADU92183 standard; protein; 137 AA.
DE Human hair keratin-associated-protein SEQ ID NO:42.
PN WO2003042387-A1.
PD 22-MAY-2003.
PA (UYKE-) UNIV KEIO.
PA (NIPR-) JAPAN SOC PROMOTION SCI.
Query Match 4.5%; Score 75.5; DB 7; Length 137;
Best Local Similarity 29.5%; Pred. No. 30;
RESULT 973
ID ABU26522 standard; protein; 213 AA.
DE Protein encoded by Prokaryotic essential gene #12049.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.5%; Score 75.5; DB 6; Length 213;
Best Local Similarity 24.2%; Pred. No. 56;
RESULT 974
ID AAU79178 standard; protein; 304 AA.
DE Human partial tandem PH-domain-containing protein-2 (TAPP2) protein.
PN WO200212276-A2.
PD 14-FEB-2002.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 4.5%; Score 75.5; DB 5; Length 304;
Best Local Similarity 25.2%; Pred. No. 93;
RESULT 975
ID AAY96079 standard; protein; 323 AA.
DE Secretable angiogenesis inhibitor p27(25-93)-p16 fusion W9.
PN WO200052158-A1.
PD 08-SEP-2000.
PA (CELL-) CELL GENESYS INC.
PA (MITO-) MITOTIX INC.
Query Match 4.5%; Score 75.5; DB 3; Length 323;
Best Local Similarity 24.0%; Pred. No. 1e+02;
RESULT 976
ID ABR40240 standard; protein; 355 AA.
DE Human TAPP2.
PN WO2003011901-A1.
PD 13-FEB-2003.
PA (UYDU-) UNIV DUNDEE.
Query Match 4.5%; Score 75.5; DB 6; Length 355;
Best Local Similarity 25.2%; Pred. No. 1.2e+02;
RESULT 977
ID AAU79175 standard; protein; 357 AA.
DE Partial human tandem PH-domain-containing protein-2 (TAPP2) protein.
PN WO200212276-A2.
PD 14-FEB-2002.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match 4.5%; Score 75.5; DB 5; Length 357;
Best Local Similarity 25.2%; Pred. No. 1.2e+02;
RESULT 978
ID ABU00587 standard; protein; 363 AA.
DE S. pneumoniae type 4 strain protein from coding region #154.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 4.5%; Score 75.5; DB 6; Length 363;
Best Local Similarity 19.9%; Pred. No. 1.2e+02;
RESULT 979
ID ADM92069 standard; protein; 363 AA.

DE S pneumoniae antigenic protein sequence SeqID266.
PN WO2004020609-A2.
PD 11-MAR-2004.
PA (TUFT) UNIV TUFTS.
Query Match 4.5%; Score 75.5; DB 8; Length 363;
Best Local Similarity 19.9%; Pred. No. 1.2e+02;
RESULT 980
ID AAY81674 standard; protein; 364 AA.
DE Streptococcus pneumoniae protein sequence ID211 - 4127.2.
PN WO200006737-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNICS LTD.
Query Match 4.5%; Score 75.5; DB 3; Length 364;
Best Local Similarity 19.9%; Pred. No. 1.2e+02;
RESULT 981
ID ADA34683 standard; protein; 376 AA.
DE Acinetobacter baumannii protein #1844.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.5%; Score 75.5; DB 6; Length 376;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 982
ID AAG29637 standard; protein; 403 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35297.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.5%; Score 75.5; DB 3; Length 403;
Best Local Similarity 21.5%; Pred. No. 1.4e+02;
RESULT 983
ID AAG29636 standard; protein; 410 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35296.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.5%; Score 75.5; DB 3; Length 410;
Best Local Similarity 21.5%; Pred. No. 1.4e+02;
RESULT 984
ID ABB91777 standard; protein; 414 AA.
DE Herbicidially active polypeptide SEQ ID NO 988.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.5%; Score 75.5; DB 5; Length 414;
Best Local Similarity 21.8%; Pred. No. 1.4e+02;
RESULT 985
ID ABM61055 standard; protein; 525 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81759, SEQ:2729.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.5%; Score 75.5; DB 8; Length 525;
Best Local Similarity 22.6%; Pred. No. 2e+02;
RESULT 986
ID ADE40118 standard; protein; 690 AA.
DE Human NOV9a protein - SEQ ID 24.
PN WO2003064589-A2.
PD 07-AUG-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.5%; Score 75.5; DB 7; Length 690;
Best Local Similarity 23.6%; Pred. No. 3e+02;
RESULT 987
ID ADN19103 standard; protein; 754 AA.
DE Bacterial polypeptide #1756.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.5%; Score 75.5; DB 8; Length 754;
Best Local Similarity 18.5%; Pred. No. 3.4e+02;
RESULT 988

ID ADI45095 standard; protein; 1162 AA.
DE Rice isoprenoid biosynthesis-associated protein #13.
PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOF/) GOF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match 4.5%; Score 75.5; DB 8; Length 1162;
Best Local Similarity 18.4%; Pred. No. 6.4e+02;
RESULT 989
ID ADS44198 standard; protein; 1284 AA.
DE Bacterial polypeptide #22628.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.5%; Score 75.5; DB 8; Length 1284;
Best Local Similarity 20.7%; Pred. No. 7.4e+02;
RESULT 990
ID AAY37230 standard; protein; 148 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GBST) GENSET.
Query Match 4.4%; Score 75; DB 2; Length 148;
Best Local Similarity 29.2%; Pred. No. 37;
RESULT 991
ID AAW79397 standard; protein; 226 AA.
DE Staphylococcus aureus protein.
PN WO9823738-A2.
PD 04-JUN-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 4.4%; Score 75; DB 2; Length 226;
Best Local Similarity 24.3%; Pred. No. 68;
RESULT 992
ID ABU16213 standard; protein; 293 AA.
DE Protein encoded by Prokaryotic essential gene #1740.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.4%; Score 75; DB 6; Length 293;
Best Local Similarity 24.3%; Pred. No. 99;
RESULT 993
ID ABM72927 standard; protein; 293 AA.
DE Staphylococcus aureus protein #2167.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 4.4%; Score 75; DB 6; Length 293;
Best Local Similarity 24.3%; Pred. No. 99;
RESULT 994
ID ABB71061 standard; protein; 345 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39975.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 75; DB 4; Length 345;
Best Local Similarity 21.1%; Pred. No. 1.3e+02;
RESULT 995
ID AAR83405 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant N890.

PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 996
ID AAR83398 standard; protein; 402 AA.
DE Humicola insolens endoglucanase.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 997
ID AAR83411 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant S37W + P39W.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 998
ID AAR83410 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant E202A.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 999
ID AAR83417 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant E150Q.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1000
ID AAR83409 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant Q399N.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1001
ID AAR83419 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant M198L.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1002
ID AAR83407 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant H123N.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1003
ID AAR83412 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant M142E.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1004
ID AAR83418 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant E334K.
PN WO9524471-A1.

PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1005
ID AAR83408 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant T385N.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1006
ID AAY67390 standard; protein; 415 AA.
DE Endoglucanase enzyme protein sequence for use in a liquid detergent.
PN EP63311-A1.
PD 11-JAN-1995.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 4.4%; Score 75; DB 2; Length 415;
Best Local Similarity 17.6%; Pred. No. 1.6e+02;
RESULT 1007
ID AAW17926 standard; protein; 415 AA.
DE Abbrading endoglucanase.
PN WO9718286-A1.
PD 22-MAY-1997.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 415;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
RESULT 1008
ID AAY56385 standard; protein; 415 AA.
DE Cellulolytic enzyme EGI amino acid sequence.
PN WO9957260-A1.
PD 11-NOV-1999.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 4.4%; Score 75; DB 3; Length 415;
Best Local Similarity 17.6%; Pred. No. 1.6e+02;
RESULT 1009
ID AAW17928 standard; protein; 435 AA.
DE Streak-reducing endoglucanase.
PN WO9718286-A1.
PD 22-MAY-1997.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.4%; Score 75; DB 2; Length 435;
Best Local Similarity 17.6%; Pred. No. 1.8e+02;
RESULT 1010
ID AAG90523 standard; protein; 453 AA.
DE C glutamicum protein fragment SEQ ID NO: 4277.
PN EPI108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 4.4%; Score 75; DB 4; Length 453;
Best Local Similarity 29.7%; Pred. No. 1.9e+02;
RESULT 1011
ID ABB53743 standard; protein; 461 AA.
DE Lactococcus lactis protein yeeg.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 4.4%; Score 75; DB 5; Length 461;
Best Local Similarity 20.8%; Pred. No. 1.9e+02;
RESULT 1012
ID ADB64684 standard; protein; 467 AA.
DE Human protein encoded by clone MESOP20004520.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.4%; Score 75; DB 7; Length 467;
Best Local Similarity 21.2%; Pred. No. 1.9e+02;
RESULT 1013
ID ABB70728 standard; protein; 472 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 38976.
PN WO200171042-A2.

PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 75; DB 4; Length 472;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1014
ID AAB53136 standard; protein; 536 AA.
DE Macaca mulatta rhadinovirus 17577 RRV ORF17 protein SEQ ID NO:29.
PN WO200028040-A2.
PD 18-MAY-2000.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match 4.4%; Score 75; DB 3; Length 536;
Best Local Similarity 23.9%; Pred. No. 2.4e+02;
RESULT 1015
ID ADA5568 standard; protein; 536 AA.
DE Human protein, SEQ ID 3136.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.4%; Score 75; DB 6; Length 536;
Best Local Similarity 20.0%; Pred. No. 2.4e+02;
RESULT 1016
ID AAB12455 standard; protein; 617 AA.
DE Human HSLy1 protein SEQ ID NO:6.
PN CN1250095-A.
PD 12-APR-2000.
PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
Query Match 4.4%; Score 75; DB 3; Length 617;
Best Local Similarity 23.0%; Pred. No. 2.9e+02;
RESULT 1017
ID AAW44162 standard; protein; 637 AA.
DE Novel protein from rat primary culture astrosite.
PN JPI0025300-A.
PD 27-JAN-1998.
PA (DAIN) DAINIPPON PHARM CO LTD.
PA (TOYA/) TOYAMA M.
Query Match 4.4%; Score 75; DB 2; Length 637;
Best Local Similarity 23.2%; Pred. No. 3e+02;
RESULT 1018
ID AAB12456 standard; protein; 637 AA.
DE RSLY1N protein sequence.
PN CN1250095-A.
PD 12-APR-2000.
PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
Query Match 4.4%; Score 75; DB 3; Length 637;
Best Local Similarity 23.2%; Pred. No. 3e+02;
RESULT 1019
ID AAY76597 standard; protein; 645 AA.
DE Human ovarian tumor EST fragment encoded protein 93.
PN DE19817557-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 4.4%; Score 75; DB 2; Length 645;
Best Local Similarity 23.0%; Pred. No. 3.1e+02;
RESULT 1020
ID ABG07430 standard; protein; 661 AA.
DE Novel human diagnostic protein #7421.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 75; DB 4; Length 661;
Best Local Similarity 20.7%; Pred. No. 3.2e+02;
RESULT 1021
ID AAB13638 standard; protein; 866 AA.
DE C. trachomatis pmpI gene amino terminus minus signal sequence protein.
PN WO200034483-A2.
PD 15-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match 4.4%; Score 75; DB 3; Length 866;
Best Local Similarity 29.2%; Pred. No. 4.7e+02;
RESULT 1022
ID AAG83206 standard; protein; 866 AA.
DE Protein encoded by Chlamydia trachomatis pmpI gene.

PN WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 4.4%; Score 75; DB 4; Length 866;
Best Local Similarity 29.2%; Pred. No. 4.7e+02;
RESULT 1023
ID ABB94177 standard; protein; 866 AA.
DE Chlamydia protein sequence SEQ ID NO:189.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 4.4%; Score 75; DB 5; Length 866;
Best Local Similarity 29.2%; Pred. No. 4.7e+02;
RESULT 1024
ID ABB91601 standard; protein; 970 AA.
DE Herbicidally active polypeptide SEQ ID NO 812.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.4%; Score 75; DB 5; Length 970;
Best Local Similarity 19.7%; Pred. No. 5.6e+02;
RESULT 1025
ID ABG25739 standard; protein; 1155 AA.
DE Novel human diagnostic protein #25730.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 75; DB 4; Length 1155;
Best Local Similarity 20.7%; Pred. No. 7.2e+02;
RESULT 1026
ID AAB24892 standard; peptide; 1199 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:403.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 4.4%; Score 75; DB 3; Length 1199;
Best Local Similarity 19.7%; Pred. No. 7.5e+02;
RESULT 1027
ID AAB24891 standard; peptide; 1210 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:402.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 4.4%; Score 75; DB 3; Length 1210;
Best Local Similarity 19.7%; Pred. No. 7.6e+02;
RESULT 1028
ID AAW19783 standard; protein; 1248 AA.
DE Human multiple regulatory protein SPT6.
PN WO9703087-A1.
PD 30-JAN-1997.
PA (UNMI) UNIV MICHIGAN.
Query Match 4.4%; Score 75; DB 2; Length 1248;
Best Local Similarity 22.4%; Pred. No. 8e+02;
RESULT 1029
ID AAB24890 standard; peptide; 1276 AA.
DE Plant SDF encoded polypeptide sequence SEQ List 1 NO:401.
PN WO200040695-A2.
PD 13-JUL-2000.
PA (CERE-) CERES INC.
Query Match 4.4%; Score 75; DB 3; Length 1276;
Best Local Similarity 19.7%; Pred. No. 8.3e+02;
RESULT 1030
ID ADN20691 standard; protein; 1310 AA.
DE Bacterial polypeptide #3344.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.4%; Score 75; DB 8; Length 1310;
Best Local Similarity 17.8%; Pred. No. 8.6e+02;

RESULT 1031
ID ABG14462 standard; protein; 353 AA.
DE Novel human diagnostic protein #14453.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 74.5; DB 4; Length 353;
Best Local Similarity 20.5%; Pred. No. 1.5e+02;
RESULT 1032
ID AAM69428 standard; protein; 378 AA.
DE Human secreted protein bp537_4.
PN WO9840404-A2.
PD 17-SEP-1998.
PA (GEMV) GENETICS INST INC.
Query Match 4.4%; Score 74.5; DB 2; Length 378;
Best Local Similarity 18.8%; Pred. No. 1.6e+02;
RESULT 1033
ID ABU24050 standard; protein; 437 AA.
DE Protein encoded by Prokaryotic essential gene #9577.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.4%; Score 74.5; DB 6; Length 437;
Best Local Similarity 19.7%; Pred. No. 2e+02;
RESULT 1034
ID ABR57280 standard; protein; 525 AA.
DE Human coronin 2A protein Coronin_2A.
PN WO2003040296-A2.
PD 15-MAY-2003.
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
PA (HAED/) HAEDER T.
Query Match 4.4%; Score 74.5; DB 6; Length 525;
Best Local Similarity 22.6%; Pred. No. 2.6e+02;
RESULT 1035
ID ABU03730 standard; protein; 539 AA.
DE Human expressed protein tag (EPT) #396.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 4.4%; Score 74.5; DB 6; Length 539;
Best Local Similarity 23.3%; Pred. No. 2.7e+02;
RESULT 1036
ID ABU03731 standard; protein; 539 AA.
DE Human expressed protein tag (EPT) #397.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 4.4%; Score 74.5; DB 6; Length 539;
Best Local Similarity 23.3%; Pred. No. 2.7e+02;
RESULT 1037
ID ABU03729 standard; protein; 539 AA.
DE Human expressed protein tag (EPT) #395.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 4.4%; Score 74.5; DB 6; Length 539;
Best Local Similarity 23.3%; Pred. No. 2.7e+02;
RESULT 1038
ID ABU03732 standard; protein; 539 AA.
DE Human expressed protein tag (EPT) #398.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 4.4%; Score 74.5; DB 6; Length 539;
Best Local Similarity 23.3%; Pred. No. 2.7e+02;
RESULT 1039
ID ADM05790 standard; protein; 595 AA.
DE Human protein of the invention SEQ ID NO:4475.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.4%; Score 74.5; DB 7; Length 595;
Best Local Similarity 23.5%; Pred. No. 3.1e+02;

RESULT 1040
ID AAE26672 standard; protein; 717 AA.
DE Human 59914 protein.
PN EP1236739-A2.
PD 04-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.4%; Score 74.5; DB 5; Length 717;
Best Local Similarity 23.0%; Pred. No. 4.1e+02;
RESULT 1041
ID ADB65311 standard; protein; 717 AA.
DE Human protein encoded by clone TESTI20070400.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.4%; Score 74.5; DB 7; Length 717;
Best Local Similarity 23.0%; Pred. No. 4.1e+02;
RESULT 1042
ID ADH51689 standard; protein; 717 AA.
DE Human 59914 protein amino acid sequence.
PN US2003219806-A1.
PD 27-NOV-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.4%; Score 74.5; DB 8; Length 717;
Best Local Similarity 23.0%; Pred. No. 4.1e+02;
RESULT 1043
ID ADR44908 standard; protein; 717 AA.
DE Polypeptide 59914 amino acid sequence.
PN WO2004071411-A2.
PD 26-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.4%; Score 74.5; DB 8; Length 717;
Best Local Similarity 23.0%; Pred. No. 4.1e+02;
RESULT 1044
ID AAW70899 standard; protein; 761 AA.
DE Protein encoded by tumour suppressor gene IB3089A.
PN WO9854318-A1.
PD 03-DEC-1998.
PA (CURT-) CURIE RES INST MARIE.
Query Match 4.4%; Score 74.5; DB 2; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;
RESULT 1045
ID AAY44704 standard; protein; 761 AA.
DE Human tumour suppressor protein IB3089A.
PN WO200001816-A1.
PD 13-JAN-2000.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 4.4%; Score 74.5; DB 3; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;
RESULT 1046
ID ADJ75380 standard; protein; 761 AA.
DE Marker gene related amino acid sequence SEQ ID NO:632.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.4%; Score 74.5; DB 8; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;
RESULT 1047
ID ADQ20487 standard; protein; 761 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3307.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.4%; Score 74.5; DB 8; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;
RESULT 1048
ID ADR14427 standard; protein; 761 AA.
DE Human NF-kappaB pathway-associated protein Segidp428.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 4.4%; Score 74.5; DB 8; Length 761;
Best Local Similarity 21.1%; Pred. No. 4.4e+02;

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RESULT 1049
ID AAB43158 standard; protein; 823 AA.
DE Human ORF2922 polypeptide sequence SEQ ID NO:5844.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
  Query Match. 4.4%; Score 74.5; DB 3; Length 823;
  Best Local Similarity 23.1%; Pred. No. 4.9e+02;
  RESULT 1050
ID ADP64439 standard; protein; 833 AA.
DE Human KM-HN-1 protein used to treat head and neck cancer Segid 1.
PN JP2004147649-A.
PD 27-MAY-2004.
PA (KUMA-) ZH KUMAMOTO TECHNO SANGYO ZAIDAN.
  Query Match. 4.4%; Score 74.5; DB 8; Length 833;
  Best Local Similarity 23.5%; Pred. No. 5e+02;
  RESULT 1051
ID AAU84380 standard; protein; 1009 AA.
DE Novel human secreted or membrane-associated protein #19.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
PA (GLAX ) GLAXO GROUP LTD.
  Query Match. 4.4%; Score 74.5; DB 5; Length 1009;
  Best Local Similarity 23.1%; Pred. No. 6.6e+02;
  RESULT 1052
ID AAE25387 standard; protein; 1009 AA.
DE Human NZMS-11 protein.
PN WO200246385-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
  Query Match. 4.4%; Score 74.5; DB 5; Length 1009;
  Best Local Similarity 23.1%; Pred. No. 6.6e+02;
  RESULT 1053
ID ADC26201 standard; protein; 1022 AA.
DE Human NOV5 protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
  Query Match. 4.4%; Score 74.5; DB 7; Length 1022;
  Best Local Similarity 23.1%; Pred. No. 6.8e+02;
  RESULT 1054
ID ADN49840 standard; protein; 1125 AA.
DE Turkey astrovirus (Tactv) ORF1a encoded serine protease.
PN US6696562-B1.
PD 24-FEB-2004.
PA (USDA ) US SEC OF AGRIC.
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
  Query Match. 4.4%; Score 74.5; DB 8; Length 1125;
  Best Local Similarity 20.7%; Pred. No. 7.8e+02;
  RESULT 1055
ID ABU35640 standard; protein; 1139 AA.
DE Protein encoded by Prokaryotic essential gene #21167.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
  Query Match. 4.4%; Score 74.5; DB 6; Length 1139;
  Best Local Similarity 23.2%; Pred. No. 7.9e+02;
  RESULT 1056
ID ABO23514 standard; protein; 1139 AA.
DE Mycoplasma genitalium outlier protein #1.
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
  Query Match. 4.4%; Score 74.5; DB 7; Length 1139;
  Best Local Similarity 23.2%; Pred. No. 7.9e+02;
  RESULT 1057
ID AAR8453 standard; protein; 1342 AA.
DE erB-3 polypeptide.
PN US5480968-A.
PD 02-JAN-1996.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
  Query Match. 4.4%; Score 74.5; DB 2; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
  RESULT 1058
ID AAW69406 standard; protein; 1342 AA.
DE ErB-3 glycoprotein clone E3-16.
PN US5820859-A.
PD 13-OCT-1998.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
  Query Match. 4.4%; Score 74.5; DB 2; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
  RESULT 1059
ID AAY16594 standard; protein; 1342 AA.
DE erB-3 protein encoded by the E3-16 cDNA clone.
PN US5916755-A.
PD 29-JUN-1999.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
  Query Match. 4.4%; Score 74.5; DB 2; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
  RESULT 1060
ID ADA37256 standard; protein; 1342 AA.
DE Human ErB3 amino acid sequence SEQ ID NO:6.
PN WO2003066677-A1.
PD 14-AUG-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (RIKE ) RIKEN KK.
PA (MOCH ) MOCHIDA PHARM CO LTD.
  Query Match. 4.4%; Score 74.5; DB 7; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
  RESULT 1061
ID ADD52685 standard; protein; 1342 AA.
DE Human erB-3.
PN US6639060-B1.
PD 28-OCT-2003.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
  Query Match. 4.4%; Score 74.5; DB 7; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
  RESULT 1062
ID ADE62708 standard; protein; 1342 AA.
DE Human Protein P21860, SEQ ID NO 8640.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
  Query Match. 4.4%; Score 74.5; DB 7; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
  RESULT 1063
ID ADE36712 standard; protein; 1342 AA.
DE Human ErB-3 amino acid sequence SEQ ID NO:1.
PN WO2003080835-A1.
PD 02-OCT-2003.
PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.
  Query Match. 4.4%; Score 74.5; DB 7; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
  RESULT 1064
ID ADM10301 standard; protein; 1342 AA.
DE Human epidermal growth factor receptor (EGFR) polypeptide #1.
PN US2003053995-A1.
PD 20-MAR-2003.
PA (HUNG/) HUNG M.
PA (LINS/) LIN S.
  Query Match. 4.4%; Score 74.5; DB 7; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
  RESULT 1065
ID ADJ6656 standard; protein; 1342 AA.
DE Her3 protein for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZOME AG.
  Query Match. 4.4%; Score 74.5; DB 8; Length 1342;
  Best Local Similarity 21.4%; Pred. No. 1e+03;
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RESULT 1066
ID ADO56208 standard; protein; 1342 AA.
DE Human ErbB-3.
PN US2004063140-A1.
PD 01-APR-2004.
PA (KRAU/) KRAUS M H.
PA (AARO/) AARONSON S A.
Query Match 4.4%; Score 74.5; DB 8; Length 1342;
Best Local Similarity 21.4%; Pred. No. 1e+03;
RESULT 1067
ID AAR12608 standard; protein; 1343 AA.
DE EGRF-R erbB-3 clone E3-16 product.
PN WO9108214-A.
PD 13-JUN-1991.
PA (USDC) US SEC OF COMMERCE.
PA (USSH) NAT INST OF HEALTH.
Query Match 4.4%; Score 74.5; DB 2; Length 1343;
Best Local Similarity 21.4%; Pred. No. 1e+03;
RESULT 1068
ID ADH48822 standard; protein; 1426 AA.
DE NOV45A protein sequence, SEQ ID 106.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.4%; Score 74.5; DB 5; Length 1426;
Best Local Similarity 21.3%; Pred. No. 1.1e+03;
RESULT 1069
ID ABB63592 standard; protein; 1513 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17568.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.4%; Score 74.5; DB 4; Length 1513;
Best Local Similarity 18.5%; Pred. No. 1.2e+03;
RESULT 1070
ID ABB44550 standard; protein; 1630 AA.
DE Human wound healing related polypeptide SEQ ID NO 7.
PN CA2325226-A1.
PD 17-MAY-2001.
PA (SWIT-) SWITCH BIOTECH AG.
Query Match 4.4%; Score 74.5; DB 4; Length 1630;
Best Local Similarity 22.6%; Pred. No. 1.3e+03;
RESULT 1071
ID ABP98331 standard; protein; 1630 AA.
DE Amino acid sequence of human HECT domain protein HECT17.
PN FR2828209-A1.
PD 07-FEB-2003.
PA (CYTO-) CYTOMICS SYSTEMS SA.
Query Match 4.4%; Score 74.5; DB 6; Length 1630;
Best Local Similarity 22.6%; Pred. No. 1.3e+03;
RESULT 1072
ID AAM39023 standard; protein; 1632 AA.
DE Human polypeptide SEQ ID NO 2168.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 74.5; DB 4; Length 1632;
Best Local Similarity 22.6%; Pred. No. 1.3e+03;
RESULT 1073
ID ADC99058 standard; protein; 2171 AA.
DE Human KRP protein - SEQ ID 11.
PN WO2003033680-A2.
PD 24-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.4%; Score 74.5; DB 7; Length 2171;
Best Local Similarity 22.6%; Pred. No. 2e+03;
RESULT 1074
ID AAR72826 standard; protein; 2482 AA.
DE Human mitosis.
PN WO9511309-A2.
PD 27-APR-1995.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 4.4%; Score 74.5; DB 2; Length 2482;

Best Local Similarity 22.0%; Pred. No. 2.4e+03;
RESULT 1075
ID AAW23996 standard; protein; 2482 AA.
DE Human mitosis amino acid sequence.
PN US5710022-A.
PD 20-JAN-1998.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 4.4%; Score 74.5; DB 2; Length 2482;
Best Local Similarity 22.0%; Pred. No. 2.4e+03;
RESULT 1076
ID ABG21509 standard; protein; 2955 AA.
DE Novel human diagnostic protein #21500.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 74.5; DB 4; Length 2955;
Best Local Similarity 22.6%; Pred. No. 3.1e+03;
RESULT 1077
ID ABB44617 standard; protein; 2988 AA.
DE Human wound healing related polypeptide SEQ ID NO 106.
PN CA2325226-A1.
PD 17-MAY-2001.
PA (SWIT-) SWITCH BIOTECH AG.
Query Match 4.4%; Score 74.5; DB 4; Length 2988;
Best Local Similarity 22.6%; Pred. No. 3.2e+03;
RESULT 1078
ID ADN95402 standard; protein; 3113 AA.
DE Human BGC/LEC-related protein sequence SeqID325.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 4.4%; Score 74.5; DB 7; Length 3113;
Best Local Similarity 22.0%; Pred. No. 3.4e+03;
RESULT 1079
ID ADK70220 standard; protein; 3113 AA.
DE Human oesophageal cancer antigen SEQ ID NO:16.
PN JP2003259872-A.
PD 16-SEP-2003.
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
Query Match 4.4%; Score 74.5; DB 8; Length 3113;
Best Local Similarity 22.0%; Pred. No. 3.4e+03;
RESULT 1080
ID ADJ72172 standard; protein; 3113 AA.
DE Human solid-cancer antigen peptide mitosis.
PN WO2004018518-A1.
PD 04-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 4.4%; Score 74.5; DB 8; Length 3113;
Best Local Similarity 22.0%; Pred. No. 3.4e+03;
RESULT 1081
ID ADQ18045 standard; protein; 3113 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 862.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.4%; Score 74.5; DB 8; Length 3113;
Best Local Similarity 22.0%; Pred. No. 3.4e+03;
RESULT 1082
ID ABU07438 standard; protein; 3210 AA.
DE Protein differentially regulated in prostate cancer #41.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 4.4%; Score 74.5; DB 6; Length 3210;
Best Local Similarity 22.0%; Pred. No. 3.5e+03;
RESULT 1083
ID ADJ66483 standard; protein; 3210 AA.
DE Cenp-F kinetochore protein for anti-cancer protein complex.
PN WO2004009622-A2.
PD 29-JAN-2004.
PA (CELL-) CELLZOME AG.
Query Match 4.4%; Score 74.5; DB 8; Length 3210;

Best Local Similarity 22.0%; Pred. No. 3.5e+03;
RESULT 1084
ID AAR9795 standard; protein; 3248 AA.
DE Kinetochore protein CENP-F.
PN WO9617867-A1.
PD 13-JUN-1996.
PA (FOXC-) FOX CHASE CANCER CENT.
PA (UYTE-) UNIV TECHNOLOGIES INT INC.
Query Match 4.4%; Score 74.5; DB 2; Length 3248;
Best Local Similarity 22.0%; Pred. No. 3.6e+03;
RESULT 1085
ID ABB49452 standard; protein; 243 AA.
DE *Listeria monocytogenes* protein #2156.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 4.4%; Score 74; DB 5; Length 243;
Best Local Similarity 21.5%; Pred. No. 96;
RESULT 1086
ID ABU32775 standard; protein; 243 AA.
DE Protein encoded by Prokaryotic essential gene #18302.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.4%; Score 74; DB 6; Length 243;
Best Local Similarity 21.5%; Pred. No. 96;
RESULT 1087
ID AAU34096 standard; protein; 286 AA.
DE *Staphylococcus aureus* cellular proliferation protein #372.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.4%; Score 74; DB 4; Length 286;
Best Local Similarity 23.7%; Pred. No. 1.2e+02;
RESULT 1088
ID AAU36606 standard; protein; 293 AA.
DE *Staphylococcus aureus* cellular proliferation protein #776.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.4%; Score 74; DB 4; Length 293;
Best Local Similarity 23.7%; Pred. No. 1.3e+02;
RESULT 1089
ID ADN72441 standard; protein; 354 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SegID 336.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDDESIGN NV.
Query Match 4.4%; Score 74; DB 8; Length 354;
Best Local Similarity 20.8%; Pred. No. 1.7e+02;
RESULT 1090
ID ADN19574 standard; protein; 423 AA.
DE Bacterial polypeptide #2227.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.4%; Score 74; DB 8; Length 423;
Best Local Similarity 22.1%; Pred. No. 2.1e+02;
RESULT 1091
ID ABP60937 standard; protein; 511 AA.
DE *Bos taurus* thioredoxin reductase SEQ ID NO:286.
PN WO200250289-A1.
PD 27-JUN-2002.
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 4.4%; Score 74; DB 5; Length 511;
Best Local Similarity 19.7%; Pred. No. 2.8e+02;
RESULT 1092
ID ABG07606 standard; protein; 557 AA.

DE Novel human diagnostic protein #7597.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.4%; Score 74; DB 4; Length 557;
Best Local Similarity 22.3%; Pred. No. 3.2e+02;
RESULT 1093
ID AAW85701 standard; protein; 628 AA.
DE Pinene synthase of grand fir.
PN WO9902030-A1.
PD 21-JAN-1999.
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
Query Match 4.4%; Score 74; DB 2; Length 628;
Best Local Similarity 21.7%; Pred. No. 3.8e+02;
RESULT 1094
ID AAY90837 standard; protein; 628 AA.
DE Grand fir pinene synthase protein sequence SEQ ID NO:20.
PN WO200017327-A2.
PD 30-MAR-2000.
PA (KENT) UNIV KENTUCKY RES DEPT.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 4.4%; Score 74; DB 3; Length 628;
Best Local Similarity 21.7%; Pred. No. 3.8e+02;
RESULT 1095
ID AAB69371 standard; protein; 628 AA.
DE Grand fir (-)-pinene synthase SEQ ID NO: 4.
PN WO200107565-A2.
PD 01-FEB-2001.
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
Query Match 4.4%; Score 74; DB 4; Length 628;
Best Local Similarity 21.7%; Pred. No. 3.8e+02;
RESULT 1096
ID ABM83344 standard; protein; 682 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3593.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.4%; Score 74; DB 8; Length 682;
Best Local Similarity 25.4%; Pred. No. 4.3e+02;
RESULT 1097
ID ABJ37047 standard; protein; 696 AA.
DE Human breast cancer / ovarian cancer related protein #23.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.4%; Score 74; DB 6; Length 696;
Best Local Similarity 20.4%; Pred. No. 4.4e+02;
RESULT 1098
ID AAU35000 standard; protein; 764 AA.
DE *Enterococcus faecalis* cellular proliferation protein #287.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.4%; Score 74; DB 4; Length 764;
Best Local Similarity 21.3%; Pred. No. 5e+02;
RESULT 1099
ID AAU33453 standard; protein; 764 AA.
DE *Enterococcus faecalis* cellular proliferation protein #89.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.4%; Score 74; DB 4; Length 764;
Best Local Similarity 21.3%; Pred. No. 5e+02;
RESULT 1100
ID ADN26543 standard; protein; 784 AA.
DE Bacterial polypeptide #9196.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

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Query Match
Best Local Similarity 26.4%; Score 74; DB 8; Length 784;
RESULT 1101
ID AAE32797 standard; protein; 1033 AA.
DE Human CEA protein.
PN WO200290508-A2.
PD 14-NOV-2002.
PA (ALPH-) ALPHAGENE INC.
Query Match
Best Local Similarity 19.9%; Score 74; DB 6; Length 1033;
RESULT 1102
ID AAU75875 standard; protein; 1049 AA.
DE SREBP2-lact fusion protein.
PN US6333167-B1.
PD 25-DEC-2001.
PA (AMHP ) AMERICAN HOME PROD CORP.
Query Match
Best Local Similarity 23.0%; Score 74; DB 5; Length 1049;
RESULT 1103
ID ADN22927 standard; protein; 1130 AA.
DE Bacterial polypeptide #5580.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 23.3%; Score 74; DB 8; Length 1130;
RESULT 1104
ID ADN22928 standard; protein; 1130 AA.
DE Bacterial polypeptide #5581.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 23.3%; Score 74; DB 8; Length 1130;
RESULT 1105
ID AAR66391 standard; protein; 1141 AA.
DE Human SREBP-2.
PN WO9426922-A2.
PD 24-NOV-1994.
PA (TEXA ) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 23.0%; Score 74; DB 2; Length 1141;
RESULT 1106
ID AAY50700 standard; protein; 1141 AA.
DE Human SREBP-2 protein.
PN DE19816902-A1.
PD 28-OCT-1999.
PA (KRON/) KRONE W.
PA (MUEL/) MUELLER-WIELAND D.
Query Match
Best Local Similarity 23.0%; Score 74; DB 2; Length 1141;
RESULT 1107
ID ABM82371 standard; protein; 1141 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO83293, SEQ.6086.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.0%; Score 74; DB 8; Length 1141;
RESULT 1108
ID ADQ39979 standard; protein; 1141 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1642.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
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Query Match
Best Local Similarity 23.8%; Score 74; DB 8; Length 1141;
RESULT 1109
ID ADQ39980 standard; protein; 1141 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1643.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 23.8%; Score 74; DB 8; Length 1141;
RESULT 1110
ID ADD48653 standard; protein; 1216 AA.
DE Rat Protein P10687, SEQ ID NO 14359.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 19.3%; Score 74; DB 7; Length 1216;
RESULT 1111
ID AAU10540 standard; protein; 1478 AA.
DE Rat CIRL-2 variant BC (YSG2) polypeptide.
PN WO200175440-A2.
PD 11-OCT-2001.
PA (WELF-) WELFIDE CORP.
Query Match
Best Local Similarity 21.9%; Score 74; DB 5; Length 1478;
RESULT 1112
ID ADD46680 standard; protein; 1478 AA.
DE Rat Protein AAC62654, SEQ ID NO 12365.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 21.9%; Score 74; DB 7; Length 1478;
RESULT 1113
ID ADE55162 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 967.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 21.9%; Score 74; DB 7; Length 1488;
RESULT 1114
ID ADE55174 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 979.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 21.9%; Score 74; DB 7; Length 1488;
RESULT 1115
ID ADE55170 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 975.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 21.9%; Score 74; DB 7; Length 1488;
RESULT 1116
ID ADE55166 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 971.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 21.9%; Score 74; DB 7; Length 1488;
RESULT 1117
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ID ABB70757 standard; protein; 143 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39063.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 73.5; DB 4; Length 143;
Best Local Similarity 18.9%; Pred. No. 51;
RESULT 1118
ID ABG12711 standard; protein; 193 AA.
DE Novel human diagnostic protein #12702.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 193;
Best Local Similarity 20.3%; Pred. No. 78;
RESULT 1119
ID ADE09966 standard; protein; 193 AA.
DE Novel protein-related contig polypeptide sequence #554.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 7; Length 193;
Best Local Similarity 20.3%; Pred. No. 78;
RESULT 1120
ID AAG13874 standard; protein; 287 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13525.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73.5; DB 3; Length 287;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1121
ID AAG13873 standard; protein; 305 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13524.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73.5; DB 3; Length 305;
Best Local Similarity 22.0%; Pred. No. 1.5e+02;
RESULT 1122
ID AAG13872 standard; protein; 312 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13523.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73.5; DB 3; Length 312;
Best Local Similarity 22.0%; Pred. No. 1.6e+02;
RESULT 1123
ID ABG14871 standard; protein; 315 AA.
DE Novel human diagnostic protein #14862.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 315;
Best Local Similarity 19.8%; Pred. No. 1.6e+02;
RESULT 1124
ID ABG22529 standard; protein; 358 AA.
DE Novel human diagnostic protein #22520.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 358;
Best Local Similarity 19.8%; Pred. No. 1.9e+02;
RESULT 1125
ID ABB47464 standard; protein; 417 AA.
DE Listeria monocytogenes protein #168.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 4.3%; Score 73.5; DB 5; Length 417;
Best Local Similarity 20.4%; Pred. No. 2.4e+02;
RESULT 1126
ID ABU32595 standard; protein; 417 AA.
DE Protein encoded by Prokaryotic essential gene #18122.
PN WO200277183-A2.
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 73.5; DB 6; Length 417;
Best Local Similarity 20.4%; Pred. No. 2.4e+02;
RESULT 1127
ID ABG01895 standard; protein; 428 AA.
DE Novel human diagnostic protein #1886.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 428;
Best Local Similarity 20.0%; Pred. No. 2.5e+02;
RESULT 1128
ID AAU91340 standard; protein; 467 AA.
DE Human novel secreted protein LP255 (b).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIT) LILLY & CO ELI.
Query Match 4.3%; Score 73.5; DB 5; Length 467;
Best Local Similarity 27.5%; Pred. No. 2.8e+02;
RESULT 1129
ID AAG21308 standard; protein; 536 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23820.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73.5; DB 3; Length 536;
Best Local Similarity 23.4%; Pred. No. 3.4e+02;
RESULT 1130
ID ABG17886 standard; protein; 833 AA.
DE Novel human diagnostic protein #17877.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73.5; DB 4; Length 833;
Best Local Similarity 19.6%; Pred. No. 6.4e+02;
RESULT 1131
ID ABB63245 standard; protein; 893 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16527.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 73.5; DB 4; Length 893;
Best Local Similarity 22.6%; Pred. No. 7.1e+02;
RESULT 1132
ID ADM04054 standard; protein; 945 AA.
DE Human protein of the invention SEQ ID NO:2739.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.3%; Score 73.5; DB 7; Length 945;
Best Local Similarity 19.1%; Pred. No. 7.7e+02;
RESULT 1133
ID ABB63754 standard; protein; 1019 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18054.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 73.5; DB 4; Length 1019;
Best Local Similarity 22.1%; Pred. No. 8.6e+02;
RESULT 1134
ID ABU40820 standard; protein; 1212 AA.
DE Protein encoded by Prokaryotic essential gene #26347.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 73.5; DB 6; Length 1212;
Best Local Similarity 22.8%; Pred. No. 1.1e+03;
RESULT 1135
ID ADO08046 standard; protein; 2845 AA.
DE Mouse polypeptide #42.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 4.3%; Score 73.5; DB 8; Length 2845;

Best Local Similarity 24.8%; Pred. No. 3.7e+03;
RESULT 1136
ID AAY56029 standard; protein; 3329 AA.
DE Human BRCA2 tumour suppressor protein.
PN WO958135-A1.
PD 18-NOV-1999.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 4.3%; Score 73.5; DB 3; Length 3329;
Best Local Similarity 21.7%; Pred. No. 4.7e+03;
RESULT 1137
ID ABUS1002 standard; protein; 189 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #345.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 4.3%; Score 73; DB 5; Length 189;
Best Local Similarity 23.5%; Pred. No. 85;
RESULT 1138
ID AAG27830 standard; protein; 269 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32820.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 269;
Best Local Similarity 22.2%; Pred. No. 1.4e+02;
RESULT 1139
ID ADQ19681 standard; protein; 276 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2500.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.3%; Score 73; DB 8; Length 276;
Best Local Similarity 19.4%; Pred. No. 1.5e+02;
RESULT 1140
ID AAG27829 standard; protein; 278 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32819.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 278;
Best Local Similarity 22.2%; Pred. No. 1.5e+02;
RESULT 1141
ID AAG53263 standard; protein; 328 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67794.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 328;
Best Local Similarity 21.5%; Pred. No. 1.9e+02;
RESULT 1142
ID ADS42868 standard; protein; 330 AA.
DE Bacterial polypeptide #21298.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 73; DB 8; Length 330;
Best Local Similarity 21.0%; Pred. No. 1.9e+02;
RESULT 1143
ID AAG53262 standard; protein; 346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67793.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 346;
Best Local Similarity 21.5%; Pred. No. 2e+02;
RESULT 1144
ID AAG53261 standard; protein; 353 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67792.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 353;
Best Local Similarity 21.5%; Pred. No. 2.1e+02;

RESULT 1145
ID ABB60115 standard; protein; 362 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7137.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 362;
Best Local Similarity 25.4%; Pred. No. 2.2e+02;
RESULT 1146
ID AAG27828 standard; protein; 376 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 32818.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 73; DB 3; Length 376;
Best Local Similarity 22.2%; Pred. No. 2.3e+02;
RESULT 1147
ID ADN26038 standard; protein; 385 AA.
DE Bacterial polypeptide #8691.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 73; DB 8; Length 385;
Best Local Similarity 19.9%; Pred. No. 2.4e+02;
RESULT 1148
ID ABUS5522 standard; protein; 446 AA.
DE Protein encoded by Prokaryotic essential gene #21049.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 73; DB 6; Length 446;
Best Local Similarity 21.1%; Pred. No. 2.9e+02;
RESULT 1149
ID ADB78618 standard; protein; 452 AA.
DE Human GABA receptor subunit mutant SEQ ID NO:162.
PN WO2003008574-A1.
PD 30-JAN-2003.
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
Query Match 4.3%; Score 73; DB 7; Length 452;
Best Local Similarity 25.9%; Pred. No. 3e+02;
RESULT 1150
ID AAY95938 standard; protein; 474 AA.
DE Porcine adenovirus 3 E1B-474R protein.
PN WO200050076-A1.
PD 31-AUG-2000.
PA (PURD) PURDUE RES FOUND.
Query Match 4.3%; Score 73; DB 3; Length 474;
Best Local Similarity 21.6%; Pred. No. 3.2e+02;
RESULT 1151
ID ADS42170 standard; protein; 479 AA.
DE Bacterial polypeptide #20600.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 73; DB 8; Length 479;
Best Local Similarity 18.8%; Pred. No. 3.3e+02;
RESULT 1152
ID ADN23648 standard; protein; 494 AA.
DE Bacterial polypeptide #6301.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.


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PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 73; DB 8; Length 494;
Best Local Similarity 19.0%; Pred. No. 3.4e+02;
RESULT 1153
ID ADF07358 standard; protein; 589 AA.
DE Bacterial polypeptide #3471.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 73; DB 7; Length 589;
Best Local Similarity 21.6%; Pred. No. 4.4e+02;
RESULT 1154
ID ABB62805 standard; protein; 635 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15207.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 635;
Best Local Similarity 19.8%; Pred. No. 4.9e+02;
RESULT 1155
ID ABO69935 standard; protein; 679 AA.
DE Pseudomonas aeruginosa polypeptide #2110.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 73; DB 7; Length 679;
Best Local Similarity 19.4%; Pred. No. 5.4e+02;
RESULT 1156
ID ABB64835 standard; protein; 692 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21297.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 692;
Best Local Similarity 24.1%; Pred. No. 5.5e+02;
RESULT 1157
ID ADR09454 standard; protein; 961 AA.
DE Human protein useful for treating neurological disease Seq 2960.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.3%; Score 73; DB 8; Length 961;
Best Local Similarity 18.4%; Pred. No. 8.9e+02;
RESULT 1158
ID ABR53657 standard; protein; 1014 AA.
DE Protein sequence #SEQ ID 2179.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 4.3%; Score 73; DB 6; Length 1014;
Best Local Similarity 16.5%; Pred. No. 9.6e+02;
RESULT 1159
ID ADK64114 standard; protein; 1014 AA.
DE Disease treating protein complex-derived protein #1318.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.3%; Score 73; DB 7; Length 1014;
Best Local Similarity 16.5%; Pred. No. 9.6e+02;
RESULT 1160
ID AAM60177 standard; protein; 1058 AA.
DE Human protein SEQ ID NO 3823.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 73; DB 4; Length 1058;
Best Local Similarity 18.4%; Pred. No. 1e+03;
RESULT 1161
ID AAM79193 standard; protein; 1216 AA.
DE Human protein SEQ ID NO 1855.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.

Query Match 4.3%; Score 73; DB 4; Length 1216;
Best Local Similarity 18.4%; Pred. No. 1.2e+03;
RESULT 1162
ID ABB08204 standard; protein; 1216 AA.
DE Human lipid metabolism enzyme-4 (LME-4).
PN WO200185956-A2.
PD 15-NOV-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.3%; Score 73; DB 5; Length 1216;
Best Local Similarity 18.4%; Pred. No. 1.2e+03;
RESULT 1163
ID ADI57184 standard; protein; 1216 AA.
DE Human PLC-beta1 protein SEQ ID NO:4.
PN WO2004007754-A2.
PD 22-JAN-2004.
PA (RIGE-) RIGBL PHARM INC.
Query Match 4.3%; Score 73; DB 8; Length 1216;
Best Local Similarity 18.4%; Pred. No. 1.2e+03;
RESULT 1164
ID AAM19785 standard; protein; 1244 AA.
DE Mouse multiple regulatory protein SPT6.
PN WO9703087-A1.
PD 30-JAN-1997.
PA (UNMT ) UNIV MICHIGAN.
Query Match 4.3%; Score 73; DB 2; Length 1244;
Best Local Similarity 22.0%; Pred. No. 1.3e+03;
RESULT 1165
ID ADC71568 standard; protein; 1548 AA.
DE Mouse subtilisin-like protein convertase 6 (SPC6).
PN US2003093824-A1.
PD 15-MAY-2003.
PA (ALLE/) ALLEN K D.
Query Match 4.3%; Score 73; DB 7; Length 1548;
Best Local Similarity 25.8%; Pred. No. 1.8e+03;
RESULT 1166
ID ABB81171 standard; protein; 1603 AA.
DE Human putative chromatin structure regulator, SUPT6H sequence.
PN WO200259606-A2.
PD 01-AUG-2002.
PA (GPCB-) GPC BIOTECH AG.
Query Match 4.3%; Score 73; DB 8; Length 1603;
Best Local Similarity 22.0%; Pred. No. 1.8e+03;
RESULT 1167
ID ADJ57844 standard; protein; 1603 AA.
DE MRB protein #16.
PN WO2004015072-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 4.3%; Score 73; DB 8; Length 1603;
Best Local Similarity 22.0%; Pred. No. 1.8e+03;
RESULT 1168
ID ABB60498 standard; protein; 1679 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8286.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 1679;
Best Local Similarity 23.6%; Pred. No. 2e+03;
RESULT 1169
ID ABB60502 standard; protein; 1679 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8298.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 4.3%; Score 73; DB 4; Length 1679;
Best Local Similarity 23.6%; Pred. No. 2e+03;
RESULT 1170
ID ADS96568 standard; protein; 1680 AA.
DE Drosophila melanogaster protein, SEQ ID 189.
PN WO2004039999-A2.
PD 13-MAY-2004.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
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Query Match 4.3%; Score 73; DB 8; Length 1680;
Best Local Similarity 23.6%; Pred. No. 2e+03;
RESULT 1171
ID ADB79869 standard; protein; 1726 AA.
DE Rat putative chromatin structure regulator, SEQ ID 109.
PN EPI279744-A2.
PD 29-JAN-2003.
PA (WARN) WARNER LAMBERT CO.
Query Match 4.3%; Score 73; DB 7; Length 1726;
Best Local Similarity 22.0%; Pred. No. 2.1e+03;
RESULT 1172
ID ABB80243 standard; protein; 1877 AA.
DE Murine subtilase.
PN WO2003060109-A2.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 73; DB 7; Length 1877;
Best Local Similarity 25.8%; Pred. No. 2.3e+03;
RESULT 1173
ID AAB35264 standard; protein; 7036 AA.
DE Human P450RAI-3 protein #1.
PN WO200295034-A2.
PD 28-NOV-2002.
PA (CYTO-) CYTOCHROMA INC.
Query Match 4.3%; Score 73; DB 6; Length 7036;
Best Local Similarity 18.9%; Pred. No. 1.6e+04;
RESULT 1174
ID AAG98340 standard; protein; 204 AA.
DE Escherichia coli protein sequence SEQ ID NO:388.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 72.5; DB 4; Length 204;
Best Local Similarity 28.2%; Pred. No. 1.1e+02;
RESULT 1175
ID ADS30663 standard; protein; 310 AA.
DE Bacterial polypeptide #19696.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 72.5; DB 8; Length 310;
Best Local Similarity 22.9%; Pred. No. 2e+02;
RESULT 1176
ID AAG52385 standard; protein; 569 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66583.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 72.5; DB 3; Length 569;
Best Local Similarity 21.2%; Pred. No. 4.7e+02;
RESULT 1177
ID AAG52384 standard; protein; 639 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66582.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 4.3%; Score 72.5; DB 3; Length 639;
Best Local Similarity 21.2%; Pred. No. 5.5e+02;
RESULT 1178
ID ABP27691 standard; protein; 750 AA.
DE Streptococcus polypeptide SEQ ID NO 4558.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 4.3%; Score 72.5; DB 5; Length 750;
Best Local Similarity 20.4%; Pred. No. 7e+02;
RESULT 1179
ID AAG52383 standard; protein; 762 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66581.
PN EPI033405-A2.

PD 06-SEP-2000.
Query Match 4.3%; Score 72.5; DB 3; Length 762;
Best Local Similarity 21.2%; Pred. No. 7.1e+02;
RESULT 1180
ID ADD78242 standard; protein; 912 AA.
DE Human CGDD-23.
PN WO2003077875-A2.
PD 25-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.3%; Score 72.5; DB 7; Length 912;
Best Local Similarity 23.8%; Pred. No. 9.3e+02;
RESULT 1181
ID ABB11773 standard; peptide; 1011 AA.
DE Human TRAP95 homologue, SEQ ID NO:2143.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 72.5; DB 4; Length 1011;
Best Local Similarity 27.5%; Pred. No. 1.1e+03;
RESULT 1182
ID AAG68179 standard; protein; 1120 AA.
DE Mitotic spindle coiled-coil related protein SEQ ID NO:95.
PN WO200177327-A1.
PD 18-OCT-2001.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 72.5; DB 4; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1183
ID ABR41103 standard; protein; 1120 AA.
DE Human mitotic spindle coiled-coil gene DEEPST protein product.
PN WO200292764-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 4.3%; Score 72.5; DB 6; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1184
ID ADB98723 standard; protein; 1120 AA.
DE Human mitotic spindle coiled-coil related protein.
PN WO200292000-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 4.3%; Score 72.5; DB 7; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1185
ID ADE82519 standard; protein; 1120 AA.
DE Human protein sequence related to the invention #9.
PN WO200292015-A2.
PD 21-NOV-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
PA (AMHP) WYETH.
Query Match 4.3%; Score 72.5; DB 7; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1186
ID ADN95291 standard; protein; 1120 AA.
DE Human BCC/LEC-related protein sequence SeqID213.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 4.3%; Score 72.5; DB 7; Length 1120;
Best Local Similarity 22.8%; Pred. No. 1.2e+03;
RESULT 1187
ID ADP06193 standard; protein; 1213 AA.
DE Bacterial polypeptide #2306.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 72.5; DB 7; Length 1213;
Best Local Similarity 22.8%; Pred. No. 1.4e+03;
RESULT 1188
ID AAM39120 standard; protein; 1246 AA.

DE Human polypeptide SEQ ID NO 2265.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.3%; Score 72.5; DB 4; Length 1246;
RESULT 1189
ID AAM40906 standard; protein; 1294 AA.
DE Human polypeptide SEQ ID NO 5837.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.3%; Score 72.5; DB 4; Length 1294;
RESULT 1190
ID AAR27819 standard; protein; 1451 AA.
DE CCVinsavc spike protein.
PN EP510773-A1.
PD 28-OCT-1992.
PA (ALKU) AKZO NV.
PA (ALKU) AKZO NOBEL NV.
Query Match
Best Local Similarity 4.3%; Score 72.5; DB 2; Length 1451;
RESULT 1191
ID ADE14361 standard; protein; 1508 AA.
DE Human intracellular signaling (INTSIG) protein #9.
PN WO2003060064-A2.
PD 24-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 4.3%; Score 72.5; DB 7; Length 1508;
RESULT 1192
ID ADN20474 standard; protein; 1970 AA.
DE Bacterial polypeptide #3127.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.3%; Score 72.5; DB 8; Length 1970;
RESULT 1193
ID ADO84848 standard; protein; 2402 AA.
DE S epidermidis surface anchored LPXTG protein SeqID20.
PN WO2004025416-A2.
PD 25-MAR-2004.
PA (TEXA) UNIV TEXAS A & M SYSTEM.
PA (INHI-) INHIBITEX INC.
PA (UABR-) UAB RES FOUND.
Query Match
Best Local Similarity 4.3%; Score 72.5; DB 8; Length 2402;
RESULT 1194
ID ADM05802 standard; protein; 278 AA.
DE Human protein of the invention SEQ ID NO:4487.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.3%; Score 72; DB 7; Length 278;
RESULT 1195
ID AAG20312 standard; protein; 310 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22450.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.3%; Score 72; DB 3; Length 310;
RESULT 1196
ID AAG38738 standard; protein; 310 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47835.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match
Best Local Similarity 4.3%; Score 72; DB 3; Length 310;
RESULT 1197
ID ABP38716 standard; protein; 315 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3561.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 4.3%; Score 72; DB 5; Length 315;
RESULT 1198
ID ADS05247 standard; protein; 315 AA.
DE Staphylococcus epidermis polypeptide seqid 4542.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 315;
RESULT 1199
ID ABB67153 standard; protein; 346 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28251.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.3%; Score 72; DB 4; Length 346;
RESULT 1200
ID ADS27474 standard; protein; 359 AA.
DE Bacterial polypeptide #16507.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 359;
RESULT 1201
ID AAM40215 standard; protein; 378 AA.
DE Human polypeptide SEQ ID NO 3360.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.3%; Score 72; DB 4; Length 378;
RESULT 1202
ID ADN26620 standard; protein; 385 AA.
DE Bacterial polypeptide #9273.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 385;
RESULT 1203
ID ADS28708 standard; protein; 387 AA.
DE Bacterial polypeptide #17741.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 387;
RESULT 1204
ID ADR86186 standard; protein; 396 AA.

DE Aspergillus fumigatus essential gene protein #236.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 4.3%; Score 72; DB 8; Length 396;
Best Local Similarity 20.6%; Pred. No. 3.1e+02;
RESULT 1205
ID AAR83413 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant K217A.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.3%; Score 72; DB 2; Length 402;
Best Local Similarity 17.6%; Pred. No. 3.2e+02;
RESULT 1206
ID AAY35620 standard; protein; 430 AA.
DE C. pneumoniae protein involved in metabolism of nucleic acids.
PN WO927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 4.3%; Score 72; DB 2; Length 430;
Best Local Similarity 23.0%; Pred. No. 3.5e+02;
RESULT 1207
ID ABB93364 standard; protein; 450 AA.
DE Herbitcically active polypeptide SEQ ID NO 2575.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 5; Length 450;
Best Local Similarity 20.1%; Pred. No. 3.8e+02;
RESULT 1208
ID ABB93037 standard; protein; 454 AA.
DE Herbitcically active polypeptide SEQ ID NO 2248.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 5; Length 454;
Best Local Similarity 19.3%; Pred. No. 3.8e+02;
RESULT 1209
ID ABB93365 standard; protein; 464 AA.
DE Herbitcically active polypeptide SEQ ID NO 2576.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 5; Length 464;
Best Local Similarity 18.3%; Pred. No. 3.9e+02;
RESULT 1210
ID ADN20815 standard; protein; 464 AA.
DE Bacterial polypeptide #3468.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 72; DB 8; Length 464;
Best Local Similarity 24.8%; Pred. No. 3.9e+02;
RESULT 1211
ID ADP47892 standard; protein; 470 AA.
DE Human CATERPILLER 11.1 nucleotide binding domain (NBD) protein.
PN WO2004034093-A2.
PD 22-APR-2004.
PA (UNNC-) UNIV NORTH CAROLINA.
Query Match 4.3%; Score 72; DB 8; Length 470;
Best Local Similarity 20.9%; Pred. No. 4e+02;
RESULT 1212
ID ADN24068 standard; protein; 470 AA.
DE Bacterial polypeptide #6721.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.3%; Score 72; DB 8; Length 470;
Best Local Similarity 20.7%; Pred. No. 4e+02;
RESULT 1213
ID AAM39422 standard; protein; 485 AA.
DE ACC synthase protein.
PN US5702933-A.
PD 30-DEC-1997.
PA (MONS) MONSANTO CO.
Query Match 4.3%; Score 72; DB 2; Length 485;
Best Local Similarity 20.3%; Pred. No. 4.2e+02;
RESULT 1214
ID ABG22476 standard; protein; 635 AA.
DE Novel human diagnostic protein #22467.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 72; DB 4; Length 635;
Best Local Similarity 20.2%; Pred. No. 6.2e+02;
RESULT 1215
ID AAO15588 standard; protein; 655 AA.
DE Human PYRIN-7 protein #2.
PN WO200261049-A2.
PD 08-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
PA (AMHP) WYETH.
Query Match 4.3%; Score 72; DB 5; Length 655;
Best Local Similarity 20.9%; Pred. No. 6.5e+02;
RESULT 1216
ID ABB07264 standard; protein; 655 AA.
DE Human APRG polypeptide (Incylte ID. 7474984CD1).
PN WO200192527-A2.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.3%; Score 72; DB 5; Length 655;
Best Local Similarity 20.9%; Pred. No. 6.5e+02;
RESULT 1217
ID ADF94751 standard; protein; 655 AA.
DE Human PYRIN-7 protein #2.
PN WO2003089588-A2.
PD 30-OCT-2003.
PA (MILL-) MILLENNIUM PHARM INC.
PA (AMHP) WYETH.
Query Match 4.3%; Score 72; DB 7; Length 655;
Best Local Similarity 20.9%; Pred. No. 6.5e+02;
RESULT 1218
ID ADJ19393 standard; protein; 655 AA.
DE Human PAN5 PAAD domain-containing full-length protein 2.
PN US2004002593-A1.
PD 01-JAN-2004.
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
Query Match 4.3%; Score 72; DB 8; Length 655;
Best Local Similarity 20.9%; Pred. No. 6.5e+02;
RESULT 1219
ID ABB61500 standard; protein; 677 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 11292.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NY.
Query Match 4.3%; Score 72; DB 4; Length 677;
Best Local Similarity 22.2%; Pred. No. 6.8e+02;
RESULT 1220
ID ABG22511 standard; protein; 692 AA.
DE Novel human diagnostic protein #22502.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 72; DB 4; Length 692;
Best Local Similarity 20.2%; Pred. No. 7e+02;

RESULT 1221
ID ABB53591 standard; protein; 712 AA.
DE Lactococcus lactis protein yciC.
PN FR2607446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 4.3%; Score 72; DB 5; Length 712;
Best Local Similarity 21.8%; Pred. No. 7.3e+02;
RESULT 1222
ID ABB68348 standard; protein; 751 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31836.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 4.3%; Score 72; DB 4; Length 751;
Best Local Similarity 20.9%; Pred. No. 7.9e+02;
RESULT 1223
ID AAV77728 standard; protein; 1021 AA.
DE Human G protein-coupled receptor HK05490.
PN WO200005264-A1.
PD 03-FEB-2000.
PA (TAKE) TAKEDA CHEM IND LTD.
PA (KAZU-) KAZUSA DNA RES INST.
Query Match 4.3%; Score 72; DB 3; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1224
ID ADE55164 standard; protein; 1021 AA.
DE Human Protein BAA34506, SEQ ID NO 969.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 7; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1225
ID ADE55168 standard; protein; 1021 AA.
DE Human Protein BAA34506, SEQ ID NO 973.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 7; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1226
ID ADE55172 standard; protein; 1021 AA.
DE Human Protein BAA34506, SEQ ID NO 977.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 7; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1227
ID ADE55176 standard; protein; 1021 AA.
DE Human Protein BAA34506, SEQ ID NO 981.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.3%; Score 72; DB 7; Length 1021;
Best Local Similarity 21.7%; Pred. No. 1.2e+03;
RESULT 1228
ID ADI17023 standard; protein; 1056 AA.
DE Human NOVX protein homologue SeqID 559.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.3%; Score 72; DB 5; Length 1056;
Best Local Similarity 22.4%; Pred. No. 1.3e+03;
RESULT 1229
ID AAY84034 standard; protein; 1109 AA.
DE Amino acid sequence of cancer associated polypeptide CH8-2a13-1.
PN WO200009655-A2.

PD 24-FEB-2000.
PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
PA (USGO) US GOVERNMENT.
Query Match 4.3%; Score 72; DB 3; Length 1109;
Best Local Similarity 19.6%; Pred. No. 1.4e+03;
RESULT 1230
ID ABU29941 standard; protein; 1173 AA.
DE Protein encoded by Prokaryotic essential gene #15468.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.3%; Score 72; DB 6; Length 1173;
Best Local Similarity 21.4%; Pred. No. 1.5e+03;
RESULT 1231
ID ADC97053 standard; protein; 1183 AA.
DE E. faecium protein sequence SEQ ID 6680.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.3%; Score 72; DB 7; Length 1183;
Best Local Similarity 21.4%; Pred. No. 1.5e+03;
RESULT 1232
ID ABC26275 standard; protein; 1459 AA.
DE Human NOV22 protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.3%; Score 72; DB 7; Length 1459;
Best Local Similarity 21.7%; Pred. No. 2.1e+03;
RESULT 1233
ID ADM97582 standard; protein; 1488 AA.
DE Human calcium-independent alpha-latrotoxin receptor.
PN WO2004031235-A1.
PD 15-APR-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 4.3%; Score 72; DB 8; Length 1488;
Best Local Similarity 21.7%; Pred. No. 2.1e+03;
RESULT 1234
ID ABG15534 standard; protein; 1909 AA.
DE Novel human diagnostic protein #15525.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.3%; Score 72; DB 4; Length 1909;
Best Local Similarity 22.8%; Pred. No. 3e+03;
RESULT 1235
ID ABM84976 standard; protein; 2104 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5225.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 2104;
Best Local Similarity 26.4%; Pred. No. 3.5e+03;
RESULT 1236
ID ABM83919 standard; protein; 3897 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4168.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 3897;
Best Local Similarity 22.9%; Pred. No. 8.4e+03;
RESULT 1237
ID ABM83916 standard; protein; 3924 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4165.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 4.3%; Score 72; DB 8; Length 3924;
Best Local Similarity 22.9%; Pred. No. 8.5e+03;
RESULT 1238
ID ABM83915 standard; protein; 3955 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4164.
PN WO2004023973-A2.

PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 3955;
RESULT 1239
ID ABM83914 standard; protein; 3985 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4163.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 3985;
RESULT 1240
ID ABM83912 standard; protein; 4016 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4161.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 4016;
RESULT 1241
ID ABM83913 standard; protein; 4072 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4162.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 4072;
RESULT 1242
ID ABM83911 standard; protein; 4082 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4160.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.3%; Score 72; DB 8; Length 4082;
RESULT 1243
ID ADL94155 standard; protein; 105 AA.
DE Human Rapr7 PHD domain amino acid sequence.
PN WO2004020581-A2.
PD 11-MAR-2004.
PA (FUNC-) FUNCTIONAL GENETICS INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 8; Length 105;
RESULT 1244
ID AAM94983 standard; protein; 118 AA.
DE Human reproductive system related antigen SEQ ID NO: 3641.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 4; Length 118;
RESULT 1245
ID ABB95691 standard; protein; 118 AA.
DE Human testicular antigen SEQ ID NO: 1075.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 4; Length 118;
RESULT 1246
ID ADJ69160 standard; protein; 205 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID966.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 7; Length 205;
RESULT 1247
ID ABG22501 standard; protein; 211 AA.
DE Novel human diagnostic protein #22492.
PN WO200175067-A2.

PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 4; Length 211;
RESULT 1248
ID ADD94810 standard; protein; 245 AA.
DE Human TREM-4-alpha protein SEQ ID NO:4.
PN WO2003080667-A2.
PD 02-OCT-2003.
PA (BIOX-) BIOXEL SPA.
PA (THOM/) THOMAS N C.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 7; Length 245;
RESULT 1249
ID ABB94329 standard; protein; 261 AA.
DE Chlamydia pneumoniae protein sequence SEQ ID NO:517.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 5; Length 261;
RESULT 1250
ID AAY37752 standard; protein; 277 AA.
DE Amino acid sequence of a Chlamydia trachomatis protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 2; Length 277;
RESULT 1251
ID AAB42989 standard; protein; 280 AA.
DE Human ORFX ORF2753 polypeptide sequence SEQ ID NO:5506.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 3; Length 280;
RESULT 1252
ID ABR53624 standard; protein; 296 AA.
DE Protein sequence #SEQ ID 2113.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 6; Length 296;
RESULT 1253
ID ADK64208 standard; protein; 296 AA.
DE Disease treating protein complex-derived protein #1271.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 7; Length 296;
RESULT 1254
ID ABM68066 standard; protein; 298 AA.
DE Photorhabdus luminescens protein sequence #1163.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 6; Length 298;
RESULT 1255
ID ADS45238 standard; protein; 322 AA.
DE Bacterial polypeptide #23668.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 8; Length 322;

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Best Local Similarity 24.1%; Pred. No. 2.6e+02;
RESULT 1256
ID ADQ62814 standard; protein; 350 AA.
DE Pseudomonas fluorescens safracin protein SacD.
PN WO2004056998-A1.
PD 08-JUL-2004.
PA (PHAR-) PHARMA MAR SA.
PA (RUFF/) RUFFLES G K.
Query Match
Best Local Similarity 22.4%; Pred. No. 3e+02;
RESULT 1257
ID ADS24938 standard; protein; 372 AA.
DE Bacterial polypeptide #13971.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 21.8%; Pred. No. 3.2e+02;
RESULT 1258
ID AAG49938 standard; protein; 380 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63228.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 24.4%; Pred. No. 3.3e+02;
RESULT 1259
ID AAG52338 standard; protein; 380 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 66520.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 24.4%; Pred. No. 3.3e+02;
RESULT 1260
ID ABUS4578 standard; protein; 457 AA.
DE Human NOVX polypeptide #37.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 18.8%; Pred. No. 4.3e+02;
RESULT 1261
ID ABB65348 standard; protein; 465 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 22836.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 20.6%; Pred. No. 4.5e+02;
RESULT 1262
ID ADJ71966 standard; protein; 581 AA.
DE Human PMM protein amino acid sequence SeqID26.
PN WO2004009797-A2.
PD 29-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 25.8%; Pred. No. 6.1e+02;
RESULT 1263
ID ABR39836 standard; protein; 590 AA.
DE Human SCAP polypeptide-Incyte Id. 71231045CD1.
PN WO2003008625-A2.
PD 30-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 23.9%; Pred. No. 6.3e+02;
RESULT 1264
ID ADO09827 standard; protein; 681 AA.
DE Hamster SGLT homologue protein SEQ ID NO:50.
PN WO2004039405-A1.
PD 13-MAY-2004.

PA (TAKE ) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 20.3%; Pred. No. 7.7e+02;
RESULT 1265
ID ABG71433 standard; protein; 683 AA.
DE Human protease polypeptide.
PN US2002137180-A1.
PD 26-SEP-2002.
PA (GANW/) GAN W.
PA (YEJU/) YE J.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match
Best Local Similarity 24.0%; Pred. No. 7.8e+02;
RESULT 1266
ID ADG62973 standard; protein; 683 AA.
DE Human protease protein.
PN US2003054489-A1.
PD 20-MAR-2003.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 24.0%; Pred. No. 7.8e+02;
RESULT 1267
ID ABR53183 standard; protein; 691 AA.
DE Protein sequence #SEQ ID 1231.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e+02;
RESULT 1268
ID ADK63218 standard; protein; 691 AA.
DE Disease treating protein complex-derived protein #735.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 22.2%; Pred. No. 7.9e+02;
RESULT 1269
ID ABP69814 standard; protein; 712 AA.
DE Human polypeptide SEQ ID NO 1861.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 22.8%; Pred. No. 8.2e+02;
RESULT 1270
ID ABM83343 standard; protein; 719 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3592.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 24.0%; Pred. No. 8.3e+02;
RESULT 1271
ID ABP97463 standard; protein; 737 AA.
DE Mouse Delta/Notch-like EGF-related receptor (DNBR).
PN WO2003029467-A1.
PD 10-APR-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match
Best Local Similarity 20.5%; Pred. No. 8.7e+02;
RESULT 1272
ID ABB59751 standard; protein; 773 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6045.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 19.8%; Pred. No. 9.3e+02;
RESULT 1273
ID ABI45257 standard; protein; 784 AA.
DE Rice isoprenoid biosynthesis-associated protein #94.
PD 13-MAY-2004.
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PN US2004010815-A1.
PD 15-JAN-2004.
PA (LANG/) LANGE B M.
PA (GHAS/) GHASSEMIAN M.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOLF/) GOLF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVART N.
PA (RICK/) RICKE D.
PA (ZHUT/) ZHU T.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 8; Length 784;
Pred. No. 9.5e+02;
RESULT 1274
ID ADD46952 standard; protein; 796 AA.
DE Rat Protein AAA41983, SEQ ID NO 12638.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEOH) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 7; Length 796;
Pred. No. 9.7e+02;
RESULT 1275
ID ADN21143 standard; protein; 958 AA.
DE Bacterial polypeptide #3796.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 8; Length 958;
Pred. No. 1.3e+03;
RESULT 1276
ID ABR53536 standard; protein; 1056 AA.
DE Protein sequence #SEQ ID 1937.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 6; Length 1056;
Pred. No. 1.5e+03;
RESULT 1277
ID ADK64418 standard; protein; 1056 AA.
DE Disease treating protein complex-derived protein #1166.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 7; Length 1056;
Pred. No. 1.5e+03;
RESULT 1278
ID ABP35715 standard; protein; 1063 AA.
DE Fungal ZBC protein sequence #141.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 5; Length 1063;
Pred. No. 1.5e+03;
RESULT 1279
ID ABP35714 standard; protein; 1068 AA.
DE Fungal ZBC protein sequence #140.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 5; Length 1068;
Pred. No. 1.5e+03;
RESULT 1280
ID ADK63116 standard; protein; 1068 AA.
DE Disease treating protein complex-derived protein #684.
PN EP1338608-A2.

PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 7; Length 1068;
Pred. No. 1.5e+03;
RESULT 1281
ID ADN23310 standard; protein; 1086 AA.
DE Bacterial polypeptide #5963.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 8; Length 1086;
Pred. No. 1.5e+03;
RESULT 1282
ID ADN21411 standard; protein; 1170 AA.
DE Bacterial polypeptide #4064.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 8; Length 1170;
Pred. No. 1.7e+03;
RESULT 1283
ID AAB62201 standard; protein; 1247 AA.
DE Cell cycle protein Radh-isoform 1.
PN WO200121784-A2.
PD 29-MAR-2001.
PA (RIGE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 4; Length 1247;
Pred. No. 1.8e+03;
RESULT 1284
ID ABG15099 standard; protein; 1607 AA.
DE Novel human diagnostic protein #15090.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 4; Length 1607;
Pred. No. 2.7e+03;
RESULT 1285
ID AAO16433 standard; protein; 1712 AA.
DE Human nucleic acid-associated protein (NAAP) - SEQ ID No 30.
PN WO2003000864-A2.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 6; Length 1712;
Pred. No. 2.9e+03;
RESULT 1286
ID ABM82532 standard; protein; 1713 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2781.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 8; Length 1713;
Pred. No. 2.9e+03;
RESULT 1287
ID AAY51843 standard; protein; 2427 AA.
DE Murine embryo macrophage m18.1 protein.
PN DE19839096-A1.
PD 02-MAR-2000.
PA (HOMA/) HOWARD J.
PA (PREF/) PREFFER K.
Query Match
Best Local Similarity 4.2%; Score 71.5; DB 3; Length 2427;
Pred. No. 4.8e+03;
RESULT 1288
ID ADJ70656 standard; protein; 2527 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2462.
PN WO2003087768-A2.

PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.2%; Score 71.5; DB 7; Length 2527;
Best Local Similarity 25.7%; Pred. No. 5.1e+03;
RESULT 1289
ID ADJ69060 standard; protein; 2715 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID866.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.2%; Score 71.5; DB 7; Length 2715;
Best Local Similarity 25.7%; Pred. No. 5.7e+03;
RESULT 1290
ID ADF45526 standard; protein; 3712 AA.
DE Pan troglodytes AKAP450 amino acid sequence.
PN WO2003102587-A1.
PD 11-DEC-2003.
PA (UYED-) UNIV EDINBURGH.
Query Match 4.2%; Score 71.5; DB 8; Length 3712;
Best Local Similarity 21.6%; Pred. No. 8.9e+03;
RESULT 1291
ID ABB53996 standard; protein; 153 AA.
DE Lactococcus lactis protein yg1B.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 4.2%; Score 71; DB 5; Length 153;
Best Local Similarity 22.3%; Pred. No. 1e+02;
RESULT 1292
ID ABU31379 standard; protein; 165 AA.
DE Protein encoded by Prokaryotic essential gene #16906.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 71; DB 6; Length 165;
Best Local Similarity 20.4%; Pred. No. 1.1e+02;
RESULT 1293
ID ABM82115 standard; protein; 182 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO83035, SEQ:5464.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.2%; Score 71; DB 8; Length 182;
Best Local Similarity 41.2%; Pred. No. 1.3e+02;
RESULT 1294
ID ABO58638 standard; protein; 191 AA.
DE Human genome derived single exon protein #5072.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 4.2%; Score 71; DB 8; Length 191;
Best Local Similarity 41.2%; Pred. No. 1.4e+02;
RESULT 1295
ID ADN99615 standard; protein; 239 AA.
DE Novel human protein sequence #431.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 4.2%; Score 71; DB 8; Length 239;
Best Local Similarity 41.2%; Pred. No. 1.9e+02;
RESULT 1296
ID ADN99614 standard; protein; 239 AA.
DE Novel human protein sequence #430.
PN WO2004038003-A2.
PD 06-MAY-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 4.2%; Score 71; DB 8; Length 239;
Best Local Similarity 41.2%; Pred. No. 1.9e+02;
RESULT 1297

ID ABO70063 standard; protein; 257 AA.
DE Pseudomonas aeruginosa polypeptide #2238.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.2%; Score 71; DB 7; Length 257;
Best Local Similarity 28.6%; Pred. No. 2.1e+02;
RESULT 1298
ID AAG31375 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37668.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.2%; Score 71; DB 3; Length 322;
Best Local Similarity 26.1%; Pred. No. 3e+02;
RESULT 1299
ID AAG31374 standard; protein; 327 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37667.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.2%; Score 71; DB 3; Length 327;
Best Local Similarity 26.1%; Pred. No. 3e+02;
RESULT 1300
ID ABB84449 standard; peptide; 327 AA.
DE Siah-related protein atSina2.
PN WO200262838-A1.
PD 15-AUG-2002.
PA (MACC-) MACCALLUM CANCER INST PETER.
PA (SVIN-) ST VINCENTS INST MEDICAL RES.
Query Match 4.2%; Score 71; DB 5; Length 327;
Best Local Similarity 26.1%; Pred. No. 3e+02;
RESULT 1301
ID ADF07575 standard; protein; 330 AA.
DE Bacterial polypeptide #3688.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.2%; Score 71; DB 7; Length 330;
Best Local Similarity 24.4%; Pred. No. 3.1e+02;
RESULT 1302
ID ABP68984 standard; protein; 399 AA.
DE Human polypeptide SEQ ID NO 1031.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 4.2%; Score 71; DB 5; Length 399;
Best Local Similarity 21.4%; Pred. No. 4e+02;
RESULT 1303
ID ABP70710 standard; protein; 399 AA.
DE Human long-chain prenyl diphosphate synthase-related protein.
PN WO200292811-A1.
PD 21-NOV-2002.
PA (KANF) KANEKA CORP.
Query Match 4.2%; Score 71; DB 6; Length 399;
Best Local Similarity 21.4%; Pred. No. 4e+02;
RESULT 1304
ID AAR83415 standard; protein; 402 AA.
DE Humicola insolens endoglucanase variant R245G.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match 4.2%; Score 71; DB 2; Length 402;
Best Local Similarity 18.2%; Pred. No. 4.1e+02;
RESULT 1305
ID ADO29463 standard; protein; 410 AA.
DE Mouse GPCR GPRC5B, SEQ ID NO:565.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 4.2%; Score 71; DB 8; Length 410;
Best Local Similarity 32.4%; Pred. No. 4.2e+02;
RESULT 1306
ID AAB43241 standard; protein; 468 AA.
DE Human ORFX ORF3005 polypeptide sequence SEQ ID NO:6010.

PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 4.2%; Score 71; DB 3; Length 468;
Best Local Similarity 18.8%; Pred. No. 5.1e+02;
RESULT 1307
ID ADU69084 standard; protein; 468 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID890.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.2%; Score 71; DB 7; Length 468;
Best Local Similarity 18.8%; Pred. No. 5.1e+02;
RESULT 1308
ID ABU49321 standard; protein; 511 AA.
DE Protein encoded by Prokaryotic essential gene #34848.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 71; DB 6; Length 511;
Best Local Similarity 20.4%; Pred. No. 5.8e+02;
RESULT 1309
ID ABR53129 standard; protein; 566 AA.
DE Protein sequence #SEQ ID 1123.
PN EPI258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 4.2%; Score 71; DB 6; Length 566;
Best Local Similarity 18.8%; Pred. No. 6.7e+02;
RESULT 1310
ID ADK62560 standard; protein; 566 AA.
DE Disease treating protein complex-derived protein #406.
PN EPI338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.2%; Score 71; DB 7; Length 566;
Best Local Similarity 18.8%; Pred. No. 6.7e+02;
RESULT 1311
ID ADI28044 standard; protein; 579 AA.
DE ECMCAD protein 4148119CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.2%; Score 71; DB 5; Length 579;
Best Local Similarity 19.3%; Pred. No. 6.9e+02;
RESULT 1312
ID ADP04513 standard; protein; 657 AA.
DE Sea squirt protein with tissue specific expression in development Seq108.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 4.2%; Score 71; DB 8; Length 657;
Best Local Similarity 19.3%; Pred. No. 8.3e+02;
RESULT 1313
ID ADI17120 standard; protein; 666 AA.
DE Human NOVX protein homologue SeqID 656.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.2%; Score 71; DB 5; Length 666;
Best Local Similarity 22.3%; Pred. No. 8.4e+02;
RESULT 1314
ID ADI17121 standard; protein; 669 AA.
DE Human NOVX protein homologue SeqID 657.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 4.2%; Score 71; DB 5; Length 669;
Best Local Similarity 22.3%; Pred. No. 8.5e+02;
RESULT 1315
ID ADQ89136 standard; protein; 669 AA.
DE Human urological disorder related protein 14303 SEQ:88.

PN WO2004065576-A2.
PD 05-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.2%; Score 71; DB 8; Length 669;
Best Local Similarity 22.3%; Pred. No. 8.5e+02;
RESULT 1316
ID ADR44922 standard; protein; 669 AA.
DE Polypeptide 14303 amino acid sequence.
PN WO2004071411-A2.
PD 26-AUG-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.2%; Score 71; DB 8; Length 669;
Best Local Similarity 22.3%; Pred. No. 8.5e+02;
RESULT 1317
ID ABB71254 standard; protein; 685 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40554.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE) PE CORP NY.
Query Match 4.2%; Score 71; DB 4; Length 685;
Best Local Similarity 20.1%; Pred. No. 8.8e+02;
RESULT 1318
ID ABM68912 standard; protein; 716 AA.
DE Photorhabdus luminescens protein sequence #2009.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.2%; Score 71; DB 6; Length 716;
Best Local Similarity 22.6%; Pred. No. 9.4e+02;
RESULT 1319
ID ADS29971 standard; protein; 751 AA.
DE Bacterial polypeptide #19004.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.2%; Score 71; DB 8; Length 751;
Best Local Similarity 22.3%; Pred. No. 1e+03;
RESULT 1320
ID ABB48512 standard; protein; 765 AA.
DE Listeria monocytogenes protein #1216.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 4.2%; Score 71; DB 5; Length 765;
Best Local Similarity 21.3%; Pred. No. 1e+03;
RESULT 1321
ID ABB91316 standard; protein; 776 AA.
DE Herbicidally active polypeptide SEQ ID NO 527.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.2%; Score 71; DB 5; Length 776;
Best Local Similarity 19.7%; Pred. No. 1.1e+03;
RESULT 1322
ID ABB93377 standard; protein; 794 AA.
DE Herbicidally active polypeptide SEQ ID NO 2588.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 4.2%; Score 71; DB 5; Length 794;
Best Local Similarity 19.5%; Pred. No. 1.1e+03;
RESULT 1323
ID AAR41869 standard; protein; 836 AA.
DE Human OSF-2.
PN EP562508-A2.
PD 29-SEP-1993.
PA (FARH) HOECHST JAPAN LTD.
Query Match 4.2%; Score 71; DB 2; Length 836;

Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1324
ID AAE06520 standard; protein; 836 AA.
DE Human OSF-2 (periostin) protein.
PN WO200157062-A1.
PD 09-AUG-2001.
PA (GENE-) GENE LOGIC INC.
Query Match 4.2%; Score 71; DB 4; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1325
ID AAU79826 standard; protein; 836 AA.
DE OSF-2 protein associated protein #4.
PN WO200220055-A1.
PD 14-MAR-2002.
PA (SUNR) SUNTORY LTD.
PA (SUNR) SUNTORY BIOMEDICAL RES LTD.
Query Match 4.2%; Score 71; DB 5; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1326
ID ABJ05566 standard; protein; 836 AA.
DE Breast cancer-associated protein 31.
PN WO200259377-A2.
PD 01-AUG-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 5; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1327
ID AAO21726 standard; protein; 836 AA.
DE Human allergy-associated protein SEQ ID NO 33.
PN WO200252006-A1.
PD 04-JUL-2002.
PA (GENO-) GENOX RES INC.
Query Match 4.2%; Score 71; DB 5; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1328
ID ABR48235 standard; protein; 836 AA.
DE Human bladder cancer associated protein sequence SEQ ID NO:191.
PN WO2003003906-A2.
PD 16-JAN-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 6; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1329
ID ABU56601 standard; protein; 836 AA.
DE Lung cancer-associated polypeptide #194.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 6; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1330
ID ABR47552 standard; protein; 836 AA.
DE Breast cancer associated protein sequence SEQ ID NO:342.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.2%; Score 71; DB 6; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1331
ID ABP96201 standard; protein; 836 AA.
DE Human osteoblast-specific factor-2 (OSF-2) protein SEQ ID NO:2.
PN WO2003016471-A2.
PD 27-FEB-2003.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 4.2%; Score 71; DB 6; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1332
ID ABR2134 standard; protein; 836 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:178.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 4.2%; Score 71; DB 6; Length 836;

Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1333
ID ADB80502 standard; protein; 836 AA.
DE Ovarian cancer-associated protein #33.
PN WO2002102235-A2.
PD 27-DEC-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 7; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1334
ID ADN38718 standard; protein; 836 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:36.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 4.2%; Score 71; DB 7; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1335
ID ADP65282 standard; protein; 836 AA.
DE Human osteoblast specific factor 2 (fasciclin I-like).
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 4.2%; Score 71; DB 7; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1336
ID ADJ75297 standard; protein; 836 AA.
DE Marker gene related amino acid sequence SEQ ID NO:549.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1337
ID ADN04500 standard; protein; 836 AA.
DE Antipsoriatic protein sequence #443.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1338
ID ADQ19060 standard; protein; 836 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1879.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1339
ID ADQ30566 standard; protein; 836 AA.
DE Pancreas cancer marker - osteoblast specific factor 2 precursor.
PN WO2004055519-A2.
PD 01-JUL-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1340
ID ADQ29664 standard; protein; 836 AA.
DE Human colorectal cancer-associated protein #19.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 4.2%; Score 71; DB 8; Length 836;
Best Local Similarity 20.3%; Pred. No. 1.2e+03;
RESULT 1341
ID ADC00978 standard; protein; 943 AA.
DE Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 1022.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.

Query Match
Best Local Similarity 4.2%; Score 71; DB 7; Length 943;
RESULT 1342
ID ABO70459 standard; protein; 1021 AA.
DE Pseudomonas aeruginosa polypeptide #2634.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 4.2%; Score 71; DB 7; Length 1021;
RESULT 1343
ID ABG28598 standard; protein; 1038 AA.
DE Novel human diagnostic protein #28589.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 71; DB 4; Length 1038;
RESULT 1344
ID ABB63423 standard; protein; 1345 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17061.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.2%; Score 71; DB 4; Length 1345;
RESULT 1345
ID ADO29116 standard; protein; 1379 AA.
DE Mouse novel GPCR LEC1, SEQ ID NO:215.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 4.2%; Score 71; DB 8; Length 1379;
RESULT 1346
ID ABP69142 standard; protein; 1759 AA.
DE Human polypeptide SEQ ID NO 1189.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 71; DB 5; Length 1759;
RESULT 1347
ID ABG15511 standard; protein; 1907 AA.
DE Novel human diagnostic protein #15502.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 71; DB 4; Length 1907;
RESULT 1348
ID ADE56175 standard; protein; 2842 AA.
DE Rat Protein P70478, SEQ ID NO 2024.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.2%; Score 71; DB 7; Length 2842;
RESULT 1349
ID AAG81395 standard; protein; 276 AA.
DE Human AFP protein sequence SEQ ID NO:308.
PN WO200129221-A2.
PD 26-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 276;
RESULT 1350
ID ADT49859 standard; protein; 282 AA.
DE Murine AKO78523(310) partial sequence/betacellulin antibody SEQ ID NO:66.
PN WO2004083241-A2.
PD 30-SEP-2004.
PA (TAKE) TAKEDA CHEM IND LTD.

Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 282;
RESULT 1351
ID ADA55092 standard; protein; 293 AA.
DE Human protein, SEQ ID 2660.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 6; Length 293;
RESULT 1352
ID ADH09610 standard; protein; 293 AA.
DE Human host factor protein, SEQ ID NO 138.
PN WO2003094847-A2.
PD 20-NOV-2003.
PA (UYEM-) UNIV EMORY.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 293;
RESULT 1353
ID AAB58346 standard; protein; 301 AA.
DE Lung cancer associated polypeptide sequence SEQ ID 684.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 3; Length 301;
RESULT 1354
ID ABG08171 standard; protein; 301 AA.
DE Novel human diagnostic protein #8162.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 301;
RESULT 1355
ID AAU39100 standard; protein; 361 AA.
DE Frog potassium-chloride cotransporter KCC.
PN WO200179525-A2.
PD 25-OCT-2001.
PA (UYVA-) UNIV VANDERBILT.
PA (GAMB/) GAMBA G.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 361;
RESULT 1356
ID ADQ95860 standard; protein; 432 AA.
DE T cell activation associated protein #19.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASahi KASEI PHARMA CORP.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 432;
RESULT 1357
ID ADC46743 standard; protein; 451 AA.
DE Thalecress transcription factor-like protein G513.
PN US2003093837-A1.
PD 15-MAY-2003.
PA (KEDD/) KEDDIE J.
PA (RIEC/) RIECHMANN J L.
PA (RATC/) RATCLIFFE O.
PA (ZHAN/) ZHANG J.
PA (JIAN/) JIANG C.
PA (PINE/) PINEDA O.
PA (HEAR/) HEARD J.
PA (YUGG/) YU G.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (REUB/) REUBER L.
PA (PILG/) PILGRIM M.
PA (SAMA/) SAMAH R.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 451;
RESULT 1358

RESULT 1358
ID ADO01911 standard; protein; 451 AA.
DE Thalecress transcription factor protein #162.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAH R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match
Best Local Similarity 22.5%; Score 70.5; DB 8; Length 451;
Pred. No. 5.4e+02;
RESULT 1359
ID ADO95862 standard; protein; 451 AA.
DE T cell activation associated protein #20.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 451;
Pred. No. 5.4e+02;
RESULT 1360
ID AAY35457 standard; protein; 453 AA.
DE Chlamydia pneumoniae involved in the secretory system.
PN WO927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 453;
Pred. No. 5.5e+02;
RESULT 1361
ID AAB85574 standard; protein; 496 AA.
DE C. pneumoniae general secretion pathway protein E polypeptide.
PN WO200121805-A1.
PD 29-MAR-2001.
PA (AVET) AVENTIS PASTEUR LTD.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 496;
Pred. No. 6.2e+02;
RESULT 1362
ID ABB54776 standard; protein; 517 AA.
DE Lactococcus lactis protein kinB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 5; Length 517;
Pred. No. 6.6e+02;
RESULT 1363
ID AAY20011 standard; protein; 524 AA.
DE B. burgdorferi antigenic protein, t301.aa.
PN WO9859071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMUNE INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 524;
Pred. No. 6.7e+02;
RESULT 1364
ID ADD14175 standard; protein; 525 AA.
DE Human src biomarker polypeptide SEQ ID NO:364.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 525;

Best Local Similarity 22.6%; Pred. No. 6.7e+02;
RESULT 1365
ID ABB47270 standard; protein; 543 AA.
DE Enterococcus faecalis polypeptide Abc8.
PN WO200179257-A2.
PD 25-OCT-2001.
PA (PHYT-) PHYTERA INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 4; Length 543;
Pred. No. 7.1e+02;
RESULT 1366
ID AAM50094 standard; protein; 547 AA.
DE Armopha-4, 11-diene synthase associated protein #2.
PN KR2001084864-A.
PD 06-SEP-2001.
PA (KIMS/) KIM S U.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 5; Length 547;
Pred. No. 7.2e+02;
RESULT 1367
ID ADI82350 standard; protein; 551 AA.
DE Artemisia annua epi-cedrol synthase protein sequence SeqID40.
PN US2004005678-A1.
PD 08-JAN-2004.
PA (KEAS/) KEASLING J.
PA (MART/) MARTIN V.
PA (PITE/) PITERA D.
PA (WITH/) WITHERS S T.
PA (NEWM/) NEWMAN J.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 551;
Pred. No. 7.2e+02;
RESULT 1368
ID AAY20010 standard; protein; 553 AA.
DE B. burgdorferi antigenic protein, f301.aa.
PN WO9859071-A1.
PD 30-DEC-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMUNE INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 553;
Pred. No. 7.3e+02;
RESULT 1369
ID ADH86572 standard; protein; 575 AA.
DE Enterococcus faecalis polypeptide #1052.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 575;
Pred. No. 7.7e+02;
RESULT 1370
ID AAR85888 standard; protein; 605 AA.
DE WD-40 domain-contg. insulin-like growth factor binding protein.
PN WO9521252-A2.
PD 10-AUG-1995.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 605;
Pred. No. 8.3e+02;
RESULT 1371
ID AAO23109 standard; protein; 605 AA.
DE IGFALS 'human modifier of p53 pathway' protein.
PN WO2003035833-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 6; Length 605;
Pred. No. 8.3e+02;
RESULT 1372
ID ADD48887 standard; protein; 605 AA.
DE Human Protein P35858, SEQ ID NO 14598.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 605;
Pred. No. 8.3e+02;
RESULT 1373

ID ADD47835 standard; protein; 605 AA.
DE Human Protein P35858, SEQ ID NO 13531.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.2%; Score 70.5; DB 7; Length 605;
Best Local Similarity 22.6%; Pred. No. 8.3e+02;
RESULT 1374
ID ADE61677 standard; protein; 605 AA.
DE Human Protein P35858, SEQ ID NO 7599.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 4.2%; Score 70.5; DB 7; Length 605;
Best Local Similarity 22.6%; Pred. No. 8.3e+02;
RESULT 1375
ID ADJ68826 standard; protein; 605 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID632.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 4.2%; Score 70.5; DB 7; Length 605;
Best Local Similarity 22.6%; Pred. No. 8.3e+02;
RESULT 1376
ID ABB54535 standard; protein; 665 AA.
DE Lactococcus lactis protein ymch.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 4.2%; Score 70.5; DB 5; Length 665;
Best Local Similarity 19.0%; Pred. No. 9.5e+02;
RESULT 1377
ID ABO76825 standard; protein; 677 AA.
DE Pseudomonas aeruginosa polypeptide #9000.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.2%; Score 70.5; DB 7; Length 677;
Best Local Similarity 20.4%; Pred. No. 9.7e+02;
RESULT 1378
ID AAR34445 standard; protein; 680 AA.
DE Sequence encoded by a cDNA clone contg. the ADMIX gene associated with X-linked Kallmann Syndrome (KS).
PN WO9307267-A1.
PD 15-APR-1993.
PA (INSP) INST PASTEUR.
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
Query Match 4.2%; Score 70.5; DB 2; Length 680;
Best Local Similarity 17.5%; Pred. No. 9.8e+02;
RESULT 1379
ID AAW49015 standard; protein; 680 AA.
DE Human KAL protein.
PN WO9824898-A2.
PD 11-JUN-1998.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 4.2%; Score 70.5; DB 2; Length 680;
Best Local Similarity 17.5%; Pred. No. 9.8e+02;
RESULT 1380
ID ADQ18482 standard; protein; 680 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1301.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.2%; Score 70.5; DB 8; Length 680;
Best Local Similarity 17.5%; Pred. No. 9.8e+02;
RESULT 1381
ID ADR09060 standard; protein; 726 AA.
DE Human protein useful for treating neurological disease Seq 2566.
PN EP1447413-A2.

PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 4.2%; Score 70.5; DB 8; Length 726;
Best Local Similarity 23.3%; Pred. No. 1.1e+03;
RESULT 1382
ID AAB68952 standard; peptide; 728 AA.
DE Arabidopsis thaliana CDC27A1 protein.
PN WO200102430-A2.
PD 11-JAN-2001.
PA (CROP-) CROPDISEGN NV.
PA (UYRI-) UNIV RIO DE JANEIRO.
Query Match 4.2%; Score 70.5; DB 4; Length 728;
Best Local Similarity 20.6%; Pred. No. 1.1e+03;
RESULT 1383
ID ADM97327 standard; protein; 728 AA.
DE A thaliana cdc27 allele 1 encoded protein.
PN WO2004029257-A1.
PD 08-APR-2004.
PA (CROP-) CROPDISEGN NV.
PA (UYRI-) UNIV RIO DE JANEIRO.
PA (HEME/) HEMERLY A S.
Query Match 4.2%; Score 70.5; DB 8; Length 728;
Best Local Similarity 20.6%; Pred. No. 1.1e+03;
RESULT 1384
ID ADR87282 standard; protein; 755 AA.
DE Liv-1 mutant BCR4M1 protein sequence.
PN WO2004067564-A2.
PD 12-AUG-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.2%; Score 70.5; DB 8; Length 755;
Best Local Similarity 18.5%; Pred. No. 1.1e+03;
RESULT 1385
ID ADG39856 standard; protein; 847 AA.
DE Protein similar to human NOV12 #2.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENNA/) PENNA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADU/) PADIGARU M.
PA (KERU/) KEKUDA R.
PA (SPYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SMIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Query Match 4.2%; Score 70.5; DB 7; Length 847;
Best Local Similarity 17.8%; Pred. No. 1.3e+03;
RESULT 1386
ID ABU36130 standard; protein; 893 AA.
DE Protein encoded by Prokaryotic essential gene #21657.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 70.5; DB 6; Length 893;
Best Local Similarity 21.5%; Pred. No. 1.4e+03;
RESULT 1387
ID ADK64818 standard; protein; 944 AA.
DE Disease treating protein complex-derived protein #1607.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.2%; Score 70.5; DB 7; Length 944;
Best Local Similarity 22.1%; Pred. No. 1.6e+03;
RESULT 1388
ID AAP97052 standard; protein; 1095 AA.
DE Sequence encoded by insecticide gene from Bacillus thuringiensis
DE israelensis strain.
PN JP01080294-A.

PD 27-MAR-1989.
PA (SUMO) SUMITOMO CHEM IND KK.
PA (MARU-) MARUBENI KK.
Query Match 4.2%; Score 70.5; DB 1; Length 1095;
Best Local Similarity 21.5%; Pred. No. 1.9e+03;
RESULT 1389
ID AAP82314 standard; protein; 1136 AA.
DE Bacillus thuringiensis 8 protein.
PN WO8806631-A.
PD 07-SEP-1988.
PA (UNMS) UNIV MICHIGAN STATE.
PA (PLAN-) PLANT GENETIC SYST.
PA (UNMI) UNIV MICHIGAN.
Query Match 4.2%; Score 70.5; DB 1; Length 1136;
Best Local Similarity 21.5%; Pred. No. 2e+03;
RESULT 1390
ID AAP93341 standard; protein; 1136 AA.
DE Sequence encoded by toxin gene derived from a Bacillus thuringiensis var.
DE israelensis (B.t.i.) microbe identified as strain HD567.
PN EP308199-A.
PD 22-MAR-1989.
PA (MYCO) MYCOGEN CORP.
Query Match 4.2%; Score 70.5; DB 1; Length 1136;
Best Local Similarity 21.5%; Pred. No. 2e+03;
RESULT 1391
ID AAU76029 standard; protein; 1136 AA.
DE Bacillus thuringiensis variant israelensis toxin (Bt8) protein sequence.
PN US6335008-B1.
PD 01-JAN-2002.
PA (UNMS) UNIV MICHIGAN STATE.
Query Match 4.2%; Score 70.5; DB 5; Length 1136;
Best Local Similarity 21.5%; Pred. No. 2e+03;
RESULT 1392
ID ADR89427 standard; protein; 1136 AA.
DE cry4Ba.
PN WO2004074462-A2.
PD 02-SEP-2004.
PA (ATHE-) ATHENIX CORP.
Query Match 4.2%; Score 70.5; DB 8; Length 1136;
Best Local Similarity 21.5%; Pred. No. 2e+03;
RESULT 1393
ID AAP82589 standard; protein; 1180 AA.
DE Insecticidal (Diptera) protein (exon 2).
PN JP63230090-A.
PD 26-SEP-1988.
PA (SUMO) SUMITOMO CHEM IND KK.
Query Match 4.2%; Score 70.5; DB 1; Length 1180;
Best Local Similarity 21.5%; Pred. No. 2.2e+03;
RESULT 1394
ID ADR89426 standard; protein; 1180 AA.
DE cry4Aa.
PN WO2004074462-A2.
PD 02-SEP-2004.
PA (ATHE-) ATHENIX CORP.
Query Match 4.2%; Score 70.5; DB 8; Length 1180;
Best Local Similarity 21.5%; Pred. No. 2.2e+03;
RESULT 1395
ID ABM81850 standard; protein; 1193 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO82709, SEQ:4766.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 4.2%; Score 70.5; DB 8; Length 1193;
Best Local Similarity 22.8%; Pred. No. 2.2e+03;
RESULT 1396
ID AAW98761 standard; protein; 1279 AA.
DE H. pylori GHP0 1090 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.2%; Score 70.5; DB 2; Length 1279;
Best Local Similarity 19.8%; Pred. No. 2.4e+03;

RESULT 1397
ID ABU07385 standard; protein; 1706 AA.
DE Human protein NOV16.
PN WO200285922-A2.
PD 31-OCT-2002.
PA (CURA-) CURAGEN CORP.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 4.2%; Score 70.5; DB 6; Length 1706;
Best Local Similarity 20.5%; Pred. No. 3.7e+03;
RESULT 1398
ID ABG91808 standard; protein; 1736 AA.
DE Human intracellular signalling molecule protein INSTIG-10.
PN WO200263008-A2.
PD 15-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 4.2%; Score 70.5; DB 5; Length 1736;
Best Local Similarity 20.5%; Pred. No. 3.8e+03;
RESULT 1399
ID ABU35589 standard; protein; 1805 AA.
DE Protein encoded by Prokaryotic essential gene #21116.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.2%; Score 70.5; DB 6; Length 1805;
Best Local Similarity 24.0%; Pred. No. 4e+03;
RESULT 1400
ID ABO23572 standard; protein; 1805 AA.
DE Mycoplasma genitalium outlier protein #3.
PN US2003039963-A1.
PD 27-FEB-2003.
PA (BRAH/) BRAHMACHARI S K.
PA (RAMA/) RAMACHANDRAN S.
PA (NAND/) NANDI T.
PA (BHIM/) BHIMARAO C.
Query Match 4.2%; Score 70.5; DB 7; Length 1805;
Best Local Similarity 24.0%; Pred. No. 4e+03;
RESULT 1401
ID AAB23012 standard; protein; 2742 AA.
DE Human APC protein (splice variant 2).
PN US6114124-A.
PD 05-SEP-2000.
PA (ICIL) IMPERIAL CHEM IND PLC.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (CANC-) CANCER INST.
Query Match 4.2%; Score 70.5; DB 3; Length 2742;
Best Local Similarity 21.8%; Pred. No. 7.3e+03;
RESULT 1402
ID AAR63508 standard; protein; 2842 AA.
DE Adenomatous polyposis coli tumour repressor.
PN US5352775-A.
PD 04-OCT-1994.
PA (ICIL) IMPERIAL CHEM IND.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
Query Match 4.2%; Score 70.5; DB 2; Length 2842;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1403
ID ABG90968 standard; peptide; 2842 AA.
DE Human APC protein.
PN US6413727-B1.
PD 02-JUL-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (NICA-) JAPANESE FOUND CANCER RES.
PA (ZENE) ZENECA LTD.
Query Match 4.2%; Score 70.5; DB 5; Length 2842;
Best Local Similarity 21.8%; Pred. No. 7.7e+03;
RESULT 1404
ID AAR26052 standard; protein; 2843 AA.
DE APC gene product in familial adenomatous polyposis.
PN WO9213103-A1.

PD 06-AUG-1992.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (ICIL) IMPERIAL CHEM IND PLC.
PA (UTAH) UNIV UTAH.
PA (CANC-) CANCER INST.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 2843;
Pred. No. 7.7e+03;
RESULT 1405
ID AAR58634 standard; protein; 2843 AA.
DE Adenomatous polypsis coli protein (APC).
PN WO9421814-A1.
PD 29-SEP-1994.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 2843;
Pred. No. 7.7e+03;
RESULT 1406
ID AAW11922 standard; protein; 2843 AA.
DE Adenomatous polypsis coli protein.
PN JP06347459-A.
PD 22-DEC-1994.
PA (SANK-) SANKO JUNYAKU CO LTD.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 2843;
Pred. No. 7.7e+03;
RESULT 1407
ID AAW35392 standard; protein; 2843 AA.
DE Human adenomatous Polypsis coli gene product.
PN US5648212-A.
PD 15-JUL-1997.
PA (NICA-) JAPANESE FOUND CANCER RES.
PA (UTAH) UNIV UTAH.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (ZENE) ZENECA LTD.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 2843;
Pred. No. 7.7e+03;
RESULT 1408
ID AAW38370 standard; protein; 2843 AA.
DE Human adenomatous Polypsis coli gene product.
PN US5691454-A.
PD 25-NOV-1997.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (ICIL) IMPERIAL CHEM IND PLC.
PA (UTAH) UNIV UTAH.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 2843;
Pred. No. 7.7e+03;
RESULT 1409
ID AAW76140 standard; protein; 2843 AA.
DE Human APC protein #1.
PN US5783666-A.
PD 21-JUL-1998.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (ZENE) ZENECA PHARM.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 2843;
Pred. No. 7.7e+03;
RESULT 1410
ID AAW76144 standard; protein; 2843 AA.
DE Human APC protein #2.
PN US5783666-A.
PD 21-JUL-1998.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (ZENE) ZENECA PHARM.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 2843;
Pred. No. 7.7e+03;
RESULT 1411
ID AAB23011 standard; protein; 2843 AA.
DE Human APC protein (splice variant 1).
PN US6114124-A.
PD 05-SEP-2000.
PA (ICIL) IMPERIAL CHEM IND PLC.

PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (CANC-) CANCER INST.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 3; Length 2843;
Pred. No. 7.7e+03;
RESULT 1412
ID ABG90964 standard; protein; 2843 AA.
DE Human adenomatous polypsis coli (APC) protein #1.
PN US6413727-B1.
PD 02-JUL-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
PA (NICA-) JAPANESE FOUND CANCER RES.
PA (ZENE) ZENECA LTD.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 5; Length 2843;
Pred. No. 7.7e+03;
RESULT 1413
ID ABG71105 standard; protein; 2843 AA.
DE Human adenomatous polypsis coli (APC) protein.
PN EP1243646-A2.
PD 25-SEP-2002.
PA (COUL) COUNCIL SCI & IND RES.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 5; Length 2843;
Pred. No. 7.7e+03;
RESULT 1414
ID ADE65846 standard; protein; 2843 AA.
DE Human adenomatosis polypsis coli protein.
PN US2003170723-A1.
PD 11-SEP-2003.
PA (SATO/) SATO T.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 2843;
Pred. No. 7.7e+03;
RESULT 1415
ID ADJ70164 standard; protein; 2843 AA.
DE Human heat mitochondrial protein as a therapeutic target SegID1970.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 7; Length 2843;
Pred. No. 7.7e+03;
RESULT 1416
ID ADJ32540 standard; protein; 2843 AA.
DE Human adenomatosis polypsis coli protein.
PN US2003224993-A1.
PD 04-DEC-2003.
PA (LAND/) LAND H.
PA (DELE/) DELEU L.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 2843;
Pred. No. 7.7e+03;
RESULT 1417
ID ADO08044 standard; protein; 2844 AA.
DE Human polypeptide #45.
PN US2004071700-A1.
PD 15-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 8; Length 2844;
Pred. No. 7.7e+03;
RESULT 1418
ID AAR63507 standard; protein; 2860 AA.
DE Adenomatous polypsis coli tumour repressor.
PN US5352775-A.
PD 04-OCT-1994.
PA (ICIL) IMPERIAL CHEM IND.
PA (CANC-) CANCER INST.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UTAH) UNIV UTAH.
Query Match
Best Local Similarity 4.2%; Score 70.5; DB 2; Length 2860;
Pred. No. 7.7e+03;
RESULT 1419
ID AAW76821 standard; protein; 2973 AA.
DE Human APC protein.
PN WO9841631-A2.

PD 24-SEP-1998.
PA (UYJO) UNIV JOHNS HOPKINS.
PA (UYUT-) RIJKSUNIV UTRECHT.
Query Match 4.2%; Score 70.5; DB 2; Length 2973;
Best Local Similarity 21.8%; Pred. No. 8.2e+03;
RESULT 1420
ID AAY70304 standard; protein; 2973 AA.
DE Protein used in cancer diagnosis associated with APC/beta-catenin.
PN WO200011195-A1.
PD 02-MAR-2000.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 4.2%; Score 70.5; DB 3; Length 2973;
Best Local Similarity 21.8%; Pred. No. 8.2e+03;
RESULT 1421
ID AAY72782 standard; protein; 2973 AA.
DE Transcriptional activation protein #1 related to the invention.
PN WO200116167-A2.
PD 08-MAR-2001.
PA (UYJO) UNIV JOHNS HOPKINS.
Query Match 4.2%; Score 70.5; DB 4; Length 2973;
Best Local Similarity 21.8%; Pred. No. 8.2e+03;
RESULT 1422
ID ABB63663 standard; protein; 3868 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17781.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 4.2%; Score 70.5; DB 4; Length 3868;
Best Local Similarity 17.6%; Pred. No. 1.2e+04;
RESULT 1423
ID ADL99351 standard; protein; 3917 AA.
DE Nanostructure assembly protein #2.
PN US2003215903-A1.
PD 20-NOV-2003.
PA (HYMA/) HYMAN P L.
PA (GOLD/) GOLDBERG E B.
Query Match 4.2%; Score 70.5; DB 8; Length 3917;
Best Local Similarity 23.0%; Pred. No. 1.2e+04;
RESULT 1424
ID AAG09240 standard; protein; 182 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7094.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 182;
Best Local Similarity 22.5%; Pred. No. 1.7e+02;
RESULT 1425
ID AAG52842 standard; protein; 182 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67215.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 182;
Best Local Similarity 22.5%; Pred. No. 1.7e+02;
RESULT 1426
ID AAY76622 standard; protein; 196 AA.
DE Human ovarian tumor EST fragment encoded protein 118.
PN DE19817557-A1.
PD 21-OCT-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 4.1%; Score 70; DB 2; Length 196;
Best Local Similarity 21.2%; Pred. No. 1.8e+02;
RESULT 1427
ID ADM48115 standard; protein; 229 AA.
DE Polypeptide sequence #165 useful in producing transgenic plants.
PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 4.1%; Score 70; DB 8; Length 229;
Best Local Similarity 21.6%; Pred. No. 2.3e+02;
RESULT 1428
ID ADM48130 standard; protein; 229 AA.
DE Polypeptide sequence #180 useful in producing transgenic plants.

PN US2003233670-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 4.1%; Score 70; DB 8; Length 229;
Best Local Similarity 21.6%; Pred. No. 2.3e+02;
RESULT 1429
ID ADJ95198 standard; protein; 232 AA.
DE Novel NOVX protein sequence #213.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.1%; Score 70; DB 7; Length 232;
Best Local Similarity 19.3%; Pred. No. 2.3e+02;
RESULT 1430
ID ADJ95190 standard; protein; 236 AA.
DE Novel NOVX protein sequence #209.
PN WO2003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match 4.1%; Score 70; DB 7; Length 236;
Best Local Similarity 19.3%; Pred. No. 2.4e+02;
RESULT 1431
ID AAG52841 standard; protein; 245 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67214.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 245;
Best Local Similarity 22.5%; Pred. No. 2.5e+02;
RESULT 1432
ID AAG09239 standard; protein; 245 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7093.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 245;
Best Local Similarity 22.5%; Pred. No. 2.5e+02;
RESULT 1433
ID ABG00390 standard; protein; 253 AA.
DE Novel human diagnostic protein #381.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 70; DB 4; Length 253;
Best Local Similarity 20.2%; Pred. No. 2.7e+02;
RESULT 1434
ID ABU44361 standard; protein; 260 AA.
DE Protein encoded by Prokaryotic essential gene #29888.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.1%; Score 70; DB 6; Length 260;
Best Local Similarity 21.9%; Pred. No. 2.8e+02;
RESULT 1435
ID AAG52840 standard; protein; 271 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67213.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 271;
Best Local Similarity 22.5%; Pred. No. 2.9e+02;
RESULT 1436
ID AAG09238 standard; protein; 271 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7092.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 4.1%; Score 70; DB 3; Length 271;
Best Local Similarity 22.5%; Pred. No. 2.9e+02;
RESULT 1437
ID ABU22933 standard; protein; 271 AA.
DE Protein encoded by Prokaryotic essential gene #8460.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match
Best Local Similarity 4.1%; Score 70; DB 6; Length 271;
RESULT 1438
ID ADH45301 standard; protein; 306 AA.
DE Human enzyme (ENZM) polypeptide, SEQ ID NO 25.
PN WO2003104410-A2.
PD 18-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 306;
RESULT 1439
ID AAG81589 standard; protein; 308 AA.
DE S. epidermidis open reading frame protein sequence SEQ ID NO:272.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 308;
RESULT 1440
ID ABP40326 standard; protein; 311 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5171.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 311;
RESULT 1441
ID ADS07667 standard; protein; 311 AA.
DE Staphylococcus epidermis polypeptide seqid 6962.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 311;
RESULT 1442
ID ABB71390 standard; protein; 366 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40962.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 366;
RESULT 1443
ID ADJ37979 standard; protein; 366 AA.
DE D melanogaster minichromosome inheritance-related protein SeqID96.
PN US2003134278-A1.
PD 17-JUL-2003.
PA (KARP/) KARPEN G H.
PA (DOBI/) DOBIE K W.
PA (COOK/) COOK K R.
PA (MURP/) MURPHY T D.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 366;
RESULT 1444
ID ABG09500 standard; protein; 386 AA.
DE Novel human diagnostic protein #9491.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 386;
RESULT 1445
ID ADA55093 standard; protein; 397 AA.
DE Human protein, SEQ ID 2661.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 6; Length 397;
RESULT 1446
ID AAR83414 standard; protein; 402 AA.

DE Humicola insolens endoglucanase variant K217A + K218T.
PN WO9524471-A1.
PD 14-SEP-1995.
PA (NOVO) NOVO-NORDISK AS.
Query Match
Best Local Similarity 4.1%; Score 70; DB 2; Length 402;
RESULT 1447
ID ADH35290 standard; protein; 417 AA.
DE ENZM protein #4.
PN WO2004003162-A2.
PD 08-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 417;
RESULT 1448
ID AAU91336 standard; protein; 423 AA.
DE Human novel secreted protein LP255(a).
PN WO200214358-A2.
PD 21-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 423;
RESULT 1449
ID ABG18976 standard; protein; 444 AA.
DE Novel human diagnostic protein #18967.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 444;
RESULT 1450
ID AAB73668 standard; protein; 468 AA.
DE Human oxidoreductase protein ORP-1.
PN WO200144448-A2.
PD 21-JUN-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 468;
RESULT 1451
ID ADJ69432 standard; protein; 468 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1238.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 468;
RESULT 1452
ID AAM23525 standard; protein; 473 AA.
DE Rabbit EST encoded protein SEQ ID NO: 1050.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 473;
RESULT 1453
ID ABP69510 standard; protein; 473 AA.
DE Human polypeptide SEQ ID NO 1557.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 473;
RESULT 1454
ID AA017865 standard; protein; 504 AA.
DE Pyrin domain containing protein NALP10/Py14.
PN WO200240668-A2.
PD 23-MAY-2002.
PA (APOT-) APOTTECH RES & DEV LTD.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 504;
RESULT 1455
ID ADE36415 standard; protein; 504 AA.

DE Human PAAD and nucleotide binding protein PANS.
PN US200307699-A1.
PD 24-APR-2003.
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (CHUZ/) CHU Z.
PA (PAWL/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (ARIZ/) ARIZA M E.
PA (STEHL) STEHLIK C.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 504;
RESULT 1456
ID ADJ19337 standard; protein; 504 AA.
DE Human PANS PAAD domain-containing full-length protein.
PN US2004002593-A1.
PD 01-JAN-2004.
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 504;
RESULT 1457
ID ADH72096 standard; protein; 579 AA.
DE Human protein of the invention NOV42k SEQ ID NO:992.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 579;
RESULT 1458
ID ADJ19403 standard; protein; 590 AA.
DE Human PANS PAAD/NACHT/ARED domain-containing protein - SEQ ID 94.
PN US2004002593-A1.
PD 01-JAN-2004.
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 590;
RESULT 1459
ID ADQ97102 standard; protein; 631 AA.
DE Human cancer associated sequence HPI-10-006, SEQ ID 78.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 631;
RESULT 1460
ID ABB63926 standard; protein; 633 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18570.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 633;
RESULT 1461
ID AAM39589 standard; protein; 639 AA.
DE Human polypeptide SEQ ID NO 2734.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 639;
RESULT 1462
ID ADP04701 standard; protein; 639 AA.
DE Sea squirt protein with tissue specific expression in development Seq296.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 639;
RESULT 1463
ID ADS21109 standard; protein; 700 AA.
DE Bacterial polypeptide #10142.

PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 700;
RESULT 1464
ID ABP97757 standard; protein; 712 AA.
DE Amino acid sequence of a murine ACDK3 polypeptide.
PN WO2003008557-A2.
PD 30-JAN-2003.
PA (UYFL) UNIV FLORIDA.
Query Match
Best Local Similarity 4.1%; Score 70; DB 6; Length 712;
RESULT 1465
ID AAB41943 standard; protein; 723 AA.
DE Human ORFX ORF1707 polypeptide sequence SEQ ID NO:3414.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 3; Length 723;
RESULT 1466
ID AAG31404 standard; protein; 727 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37707.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.1%; Score 70; DB 3; Length 727;
RESULT 1467
ID ABB93080 standard; protein; 727 AA.
DE Herbicidally active polypeptide SEQ ID NO 2291.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.1%; Score 70; DB 5; Length 727;
RESULT 1468
ID AAG31683 standard; protein; 770 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38090.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 4.1%; Score 70; DB 3; Length 770;
RESULT 1469
ID ABM85165 standard; protein; 777 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5414.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 777;
RESULT 1470
ID ABU08709 standard; protein; 786 AA.
DE Alzheimer's disease associated gene screening related Notch1 protein.
PN WO2003012141-A1.
PD 13-FEB-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
PA (NICH-) JAPAN SEC CHUBU NAT HOSPITAL.
PA (KOMA/) KOMANO H.
Query Match
Best Local Similarity 4.1%; Score 70; DB 6; Length 786;
RESULT 1471
ID ADB61453 standard; protein; 786 AA.
DE Amyloid beta related 786 amino acid protein.
PN WO2003048204-A1.
PD 12-JUN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
PA (NICH-) JAPAN SEC CHUBU NAT HOSPITAL.
PA (KOMA/) KOMANO H.

Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 786;
RESULT 1472
ID ADF53262 standard; protein; 786 AA.
DE Mouse Notch1 NCID intracellular domain.
PN JP2003289881-A.
PD 14-OCT-2003.
PA (KOKU-) KOKURITSU RYOYOJO CHUBU BYOINCHO.
PA (KOMA/) KOMANO H.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 786;
RESULT 1473
ID ADQ82206 standard; protein; 786 AA.
DE Mouse Notch 1 protein intracellular domain - NICD.
PN JP2004215517-A.
PD 05-AUG-2004.
PA (KOKU-) KOKURITSU RYOYOJO CHUBU BYOINCHO.
PA (KOMA/) KOMANO H.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 786;
RESULT 1474
ID ABB61944 standard; protein; 878 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12624.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 878;
RESULT 1475
ID AAE06695 standard; protein; 888 AA.
DE Arabidopsis thaliana ethylene-overproducer1 (ETOL)-like protein 1 (EOL1).
PN WO200157063-A1.
PD 09-AUG-2001.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 888;
RESULT 1476
ID ADN72911 standard; protein; 888 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SegID 806.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 888;
RESULT 1477
ID ADN73171 standard; protein; 888 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SegID 1066.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 888;
RESULT 1478
ID ADL22728 standard; protein; 938 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 177.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 938;
RESULT 1479
ID ADQ66760 standard; protein; 978 AA.
DE Novel human protein sequence #1733.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 978;
RESULT 1480
ID ABM83330 standard; protein; 1002 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3579.

PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 1002;
RESULT 1481
ID ABB63556 standard; protein; 1006 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17460.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 4; Length 1006;
RESULT 1482
ID ADQ66747 standard; protein; 1012 AA.
DE Novel human protein sequence #1720.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 1012;
RESULT 1483
ID ABM84874 standard; protein; 1025 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5123.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 4.1%; Score 70; DB 8; Length 1025;
RESULT 1484
ID ADE62760 standard; protein; 1085 AA.
DE Rat Protein AAC52634, SEQ ID NO 8693.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 1085;
RESULT 1485
ID ADE62756 standard; protein; 1085 AA.
DE Rat Protein AAC52634, SEQ ID NO 8689.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 1085;
RESULT 1486
ID ADE62752 standard; protein; 1085 AA.
DE Rat Protein AAC52634, SEQ ID NO 8685.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 4.1%; Score 70; DB 7; Length 1085;
RESULT 1487
ID ABU09232 standard; protein; 1167 AA.
DE Rat neuropathic pain gene 4, NPG4, polypeptide.
PN UG2003003538-A1.
PD 02-JAN-2003.
PA (DIET/) DIETRICH P S.
PA (HUAN/) HUANG C.
PA (JOHN/) JOHNSON C D.
PA (SANG/) SANGAMESWARAN L.
Query Match
Best Local Similarity 4.1%; Score 70; DB 6; Length 1167;
RESULT 1488
ID ABR53027 standard; protein; 1358 AA.
DE Protein sequence #SEQ ID 919.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.

Query Match 4.1%; Score 70; DB 6; Length 1358;
Best Local Similarity 18.0%; Pred. No. 3e+03;
RESULT 1489
ID ADK62848 standard; protein; 1358 AA.
DE Disease treating protein complex-derived protein #550.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.1%; Score 70; DB 7; Length 1358;
Best Local Similarity 18.0%; Pred. No. 3e+03;
RESULT 1490
ID ADN19005 standard; protein; 1358 AA.
DE Bacterial polypeptide #1658.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.1%; Score 70; DB 8; Length 1358;
Best Local Similarity 18.0%; Pred. No. 3e+03;
RESULT 1491
ID ABR52895 standard; protein; 1748 AA.
DE Protein sequence #SEQ ID 655.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 4.1%; Score 70; DB 6; Length 1748;
Best Local Similarity 23.3%; Pred. No. 4.3e+03;
RESULT 1492
ID ADK62418 standard; protein; 1748 AA.
DE Disease treating protein complex-derived protein #335.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.1%; Score 70; DB 7; Length 1748;
Best Local Similarity 23.3%; Pred. No. 4.3e+03;
RESULT 1493
ID ADN19312 standard; protein; 1748 AA.
DE Bacterial polypeptide #1965.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.1%; Score 70; DB 8; Length 1748;
Best Local Similarity 23.3%; Pred. No. 4.3e+03;
RESULT 1494
ID ADN24076 standard; protein; 1956 AA.
DE Bacterial polypeptide #6729.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.1%; Score 70; DB 8; Length 1956;
Best Local Similarity 20.8%; Pred. No. 5e+03;
RESULT 1495
ID ABR53118 standard; protein; 2000 AA.
DE Protein sequence #SEQ ID 1101.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 4.1%; Score 70; DB 6; Length 2000;
Best Local Similarity 22.7%; Pred. No. 5.2e+03;
RESULT 1496
ID ADK62826 standard; protein; 2000 AA.
DE Disease treating protein complex-derived protein #539.

PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 4.1%; Score 70; DB 7; Length 2000;
Best Local Similarity 22.7%; Pred. No. 5.2e+03;
RESULT 1497
ID ADN72303 standard; protein; 2009 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SegID 198.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPPDESIGN NV.
Query Match 4.1%; Score 70; DB 8; Length 2009;
Best Local Similarity 20.8%; Pred. No. 5.2e+03;
RESULT 1498
ID AD058587 standard; protein; 2531 AA.
DE Mouse Notch-1 protein, SEQ ID NO:5.
PN WO2004048578-A1.
PD 10-JUN-2004.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 4.1%; Score 70; DB 8; Length 2531;
Best Local Similarity 22.7%; Pred. No. 7.3e+03;
RESULT 1499
ID ABB48232 standard; protein; 152 AA.
DE Listeria monocytogenes protein #936.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 4.1%; Score 69.5; DB 5; Length 152;
Best Local Similarity 24.7%; Pred. No. 1.4e+02;
RESULT 1500
ID ABG05308 standard; protein; 204 AA.
DE Novel human diagnostic protein #5299.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 4.1%; Score 69.5; DB 4; Length 204;
Best Local Similarity 20.5%; Pred. No. 2.2e+02;

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